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(57) Abstract

The invention features a method for identifying a cDNA nucleic acid encoding a mammalian protein having a signal sequence, which method includes the following steps: a) providing library of mammalian cDNA; b) ligating the library of mammalian cDNA to DNA encoding alkaline phosphatase lacking both a signal sequence and a membrane anchor sequence to form ligated DNA; c) transforming bacterial cells with the ligated DNA to create a bacterial cell clone library; d) isolating DNA comprising the mammalian cDNA from at least one clone in the bacterial cell clone library; e) separately transfecting DNA isolated from clones in step (d) into mammalian cells which do not express alkaline phosphatase to create a mammalian cell clone library wherein each clone in the mammalian cell clone library corresponds to a clone in the bacterial cell clone library; f) identifying a clone in the mammalian cell clone library which express alkaline phosphatase; g) identifying the clone in the bacterial cell clone library corresponding to the clone in the mammalian cell clone library identified in step (f); and h) isolating and sequencing a portion of the mammalian cDNA present in the bacterial cell library clone identified in step (g) to identify a mammalian cDNA encoding a mammalian protein having a signal sequence.

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METHOD FOR IDENTIFYING GENES ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEINS

Background of the Invention

The invention relates to methods for identifying genes encoding novel proteins.

There is considerable medical interest in secreted and membrane-associated mammalian proteins. Many such proteins, for example, cytokines, are important for inducing the growth or differentiation of cells with which they interact or for triggering one or more specific cellular responses.

An important goal in the design and development of new therapies is the identification and characterization of secreted proteins and the genes which encode them. Traditionally, this goal has been pursued by identifying a particular response of a particular cell type and attempting to isolate and purify a secreted protein capable of eliciting the response. This approach is limited by a number of factors. First, certain secreted proteins will not be identified because the responses they evoke may not be recognizable or measurable. Second, because *in vitro* assays must be used to isolate and purify secreted proteins, somewhat artificial systems must be used. This raises the possibility that certain important secreted proteins will not be identified unless the features of the *in vitro* system (e.g., cell line, culture medium, or growth conditions) accurately reflect the *in vivo* milieu. Third, the complexity of the effects of secreted proteins on the cells with which they interact vastly complicates the task of isolating important secreted proteins. Any given cell can be simultaneously subject to the effects of two or more secreted proteins. Because any two secreted proteins

will not have the same effect on a given cell and because the effect of a first secreted protein on a given cell can alter the effect of a second secreted protein on the same cell, it can be difficult to isolate the secreted protein or proteins responsible for a given physiological response. In addition, certain secreted and membrane-associated proteins may be expressed at levels that are too low to detect by biological assay or protein purification.

In another approach, genes encoding secreted proteins have been isolated using DNA probes or PCR oligonucleotides which recognize sequence motifs present in genes encoding known secreted protein. In addition, homology-directed searching of Expressed Sequence Tag (EST) sequences derived by high-throughput sequencing of specific cDNA libraries has been used to identify genes encoding secreted proteins. These approaches depend for their success on a high degree of similarity between the DNA sequences used as probes and the unknown genes or EST sequences.

More recently, methods have been developed that permit the identification of cDNAs encoding a signal sequence capable of directing the secretion of a particular protein from certain cell types. Both Honjo, U.S. Patent No. 5,525,486, and Jacobs, U.S. Patent No. 5,536,637, describe such methods. These methods are said to be capable of identifying secreted proteins.

The demonstrated clinical utility of several secreted proteins in the treatment of human disease, for example, erythropoietin, granulocyte-macrophage colony stimulating factor (GM-CSF), human growth hormone, and various interleukins, has generated considerable interest in the identification of novel secreted proteins. The method of the invention can be employed as a tool in the discovery of such novel proteins.

Summary of the Invention

The invention features a method for isolating cDNAs and identifying encode secreted or membrane-associated (e.g. transmembrane) mammalian proteins. The method of the invention relies upon the observation that the majority of secreted and membrane-associated proteins possess at their amino termini a stretch of hydrophobic amino acid residues referred to as the "signal sequence." The signal sequence directs secreted and membrane-associated proteins to a sub-cellular membrane compartment termed the endoplasmic reticulum, from which these proteins are dispatched for secretion or presentation on the cell surface.

The invention describes a method in which oDNAs that encode signal sequences for secreted or membrane-associated proteins are isolated by virtue of their abilities to direct the export of the reporter protein, alkaline phosphatase (AP), from mammalian cells. The present method has major advantages over other signal peptide trapping approaches. The present method is highly sensitive. This facilitates the isolation of signal peptide associated proteins that may be difficult to isolate with other techniques. Moreover, the present method is amenable to throughput screening techniques and automation. Combined with a novel method for cDNA library construction in which directional random primed cDNA libraries are prepared, the invention comprises a powerful and approach to the large scale isolation of novel secreted proteins.

The invention features a method for identifying a cDNA nucleic acid encoding a mammalian protein having a signal sequence, which method includes the following steps:

a) providing library of mammalian cDNA;

b) ligating the library of mammalian cDNA to DNA encoding alkaline phosphatase lacking both a signal sequence and a membrane anchor sequence to form ligated DNA;

c) transforming bacterial cells with the ligated DNA to create a bacterial cell clone library;

d) isolating DNA comprising the mammalian cDNA from at least one clone in the bacterial cell clone library;

e) separately transfecting DNA isolated from clones in step (d) into mammalian cells which do not express alkaline phosphatase to create a mammalian cell clone library wherein each clone in the mammalian cell clone library corresponds to a clone in the bacterial cell clone library;

f) identifying a clone in the mammalian cell clone library which express alkaline phosphatase;

g) identifying the clone in the bacterial cell clone library corresponding to the clone in the mammalian cell clone library identified in step (f); and

h) isolating and sequencing a portion of the mammalian cDNA present in the bacterial cell library clone identified in step (g) to identify a mammalian cDNA encoding a mammalian protein having a signal sequence.

A cDNA library is a collection of nucelic acid molecueles that are a cDNA copy of a sample of mRNA.

In another aspect, the invention features ptrAP3 expression vector.

In another aspect, the invention features a substantially pure preparation of ethb0018f2 protein. Preferably, the ethb0018f2 protein includes an amino acid sequence substantially identical to the amino acid sequence shown in FIG. 5 (SEQ ID NO: 5); is derived from a mammal, for example, a human.

The invention also features purified DNA (for example, cDNA) which includes a sequence encoding a ethb0018f2 protein, preferably encoding a human ethb0018f2 protein (for example, the ethb0018f2 protein of FIG. 5; SEQ ID NO:5); a vector and a cell which includes a purified DNA of the invention; and a method of producing a recombinant ethb0018f2 protein involving providing a cell transformed with DNA encoding ethb0018f2 protein positioned for expression in the cell, culturing the transformed cell under conditions for expressing the DNA, and isolating the recombinant ethb0018f2 protein. The invention further features recombinant ethb0018f2 protein produced by such expression of a purified DNA of the invention.

By "ethb0018f2 protein" is meant a polypeptide which has a biological activity possesed by naturally-occuring ethb0018f2 protein. Preferably, such a polypeptide has an amino acid sequence which is at least 85%, preferably 90%, and most preferably 95% or even 99% identical to the amino acid sequence of the ethb0018f2 protein of FIG. 5 (SEQ ID NO: 5).

By "substantially identical" is meant a polypeptide or nucleic acid having a sequence that is at least 85%, preferably 90%, and more preferably 95% or more identical to the sequence of the reference amino acid or nucleic acid sequence. For polypeptides, the length of the reference polypeptide sequence will generally be at least 16 amino acids, preferably at least 20 amino acids, more preferably at least 25 amino acids, and most preferably 35 amino acids. For nucleic acids, the length of the reference nucleic acid sequence will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 110 nucleotides.

Sequence identity can be measured using sequence analysis software (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705).

In the case of polypeptide sequences which are less than 100% identical to a reference sequence, the non-identical positions are preferably, but not necessarily, conservative substitutions for the reference sequence. Conservative substitutions typically include substitutions within the following groups: glycine and alanine; valine, isoleucine, and leucine; aspartic acid and glutamic acid; asparagine and glutamine; serine and threonine; lysine and arginine; and phenylalanine and tyrosine.

Where a particular polypeptide is the to have a specific percent identity to a reference polypeptide of a defined length, the percent identity is relative to the reference peptide. Thus, a peptide that is 50% identical to a reference polypeptide that is 100 amino acids long can be a 50 amino acid polypeptide that is completely identical to a 50 amino acid long portion of the reference polypeptide. It might also be a 100 amino acid long polypeptide which is 50% identical to the reference polypeptide over its entire length. Of course, many other polypeptides will meet the same criteria.

By "protein" and "polypeptide" is meant any chain of amino acids, regardless of length or post-translational modification (e.g., glycosylation or phosphorylation).

By "substantially pure" is meant a preparation which is at least 60% by weight (dry weight) the compound of interest, i.e., a ethb0018f2 protein. Preferably the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight the

compound of interest. Purity can be measured by any appropriate method, e.g., column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

By "purified DNA" is meant DNA that is not immediately contiguous with both of the coding sequences with which it is immediately contiguous (one on the 5' end and one on the 3' end) in the naturally occurring genome of the organism from which it is derived. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector; into an autonomously replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence.

By "substantially identical" is meant an amino acid sequence which differs only by conservative amino acid substitutions, for example, substitution of one amino acid for another of the same class (e.g., valine for glycine, arginine for lysine, etc.) or by one or more non-conservative substitutions, deletions, or insertions located at positions of the amino acid sequence which do not destroy the function of the protein (assayed, e.g., as described herein). Preferably, such a sequence is at least 85%, more preferably 90%, and most preferably 95% identical at the amino acid level to the sequence of FIG. 5 (SEQ ID NO: 5). For nucleic acids, the length of comparison sequences will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 110 nucleotides. A "substantially identical" nucleic acid sequence codes for a substantially identical amino acid sequence as defined above.

By "transformed cell" is meant a cell into which (or into an ancestor of which) has been introduced, by means of recombinant DNA techniques, a DNA molecule encoding (as used herein) ethb0018f2 protein.

By "positioned for expression" is meant that the DNA molecule is positioned adjacent to a DNA sequence which directs transcription and translation of the sequence (i.e., facilitates the production of ethb0018f2 protein).

By "purified antibody" is meant antibody which is at least 60%, by weight, free from the proteins and naturally-occurring organic molecules with which it is naturally associated. Preferably, the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, antibody.

By "specifically binds" is meant an antibody which recognizes and binds ethb0018f2 protein but which does not substantially recognize and bind other molecules in a sample, e.g., a biological sample, which naturally includes ethb0018f2 protein.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

Brief Description of the Drawings

Figure 1 is a schematic drawing of a portion of the ptrAP3 vector.

Figure 2 is a representation of the DNA sequence of the ptrAP3 vector (SEQ ID NO:1). The bold, underlined portion is the small fragment removed prior to cDNA insertion sequence. The italic, underlined portion is the alkaline phosphatase sequence.

Figure 3 is a representation of the amino acid sequence of human placental alkaline phosphatase (Accession No. P05187). The underlined portion is the signal sequence. The bold, underlined portion is the membrane anchor sequence.

Figure 4 is a representation of the amino acid sequence of the alkaline phosphatase encoded by ptrAP3.

Figure 5 is a representation of the cDNA and amino acid sequence of a portion of a novel secreted protein identified using the method described in Example 1.

Figure 6 is a representation of an alignment of the amino acid sequence of clone ethb0018f2 (referred to here as 8f2) and proteins containing conserved IgG domains. The proteins are D38492 (neural adhesion molecule f3); P20241EURO (Drosophila Neuroglian); P32004EURA (human neural adhesion molecule L1); P35331G-CA (chick neural adhesion molecule related protein); Q02246XONI (human Axonin 1); U11031 (rat neural adhesion molecule BIG1); and X65224 (chicken Neurofascin) are depicted. In this figure, conserved motifs within the IgG domain are highlighted in bold.

Detailed Description

In general terms, the method of the invention entails the following steps:

1. Preparation of a randomly primed cDNA library using cDNA prepared from mRNA extracted from mammalian cells or tissue. The cDNA is inserted into a mammalian expression vector adjacent to a cDNA encoding placental alkaline phosphatase which lacks a secretory signal.

2. Amplification of the cDNA library in bacteria.

3. Isolation of the cDNA library.

4. Transfection of the resulting cDNA library into mammalian cells.

5. Assay of supernatants from the transfected mammalian cells for alkaline phosphatase activity.

6. Isolation and sequencing of plasmid DNA clones registering a positive score in the alkaline phosphatase assay.

7. Isolation of full length cDNA clones of novel proteins having a signal sequence.

The mammalian cDNA used to create the cDNA library can be prepared using any known method. Generally, the cDNA is produced from mRNA. The mRNA can be isolated from any desired tissue or cell type. For example, peripheral blood cells, primary cells, tumor cells, or other cells may be used as a source of mRNA.

The expression vector harboring the modified alkaline phosphatase gene can be any vector suitable for expression of proteins in mammalian cells.

The mammalian cells used in the transfection step can be any suitable mammalian cells, e.g., CHO cells, mouse L cells, Hela cells, VERO cells, mouse 3T3 cells, and 293 cells.

Described below is a specific example of the method of the invention. Also described below are two

genes, one known and one novel, identified using this method.

Example I

Step 1 Generation of Mammalian Signal Peptide Trap cDNA Libraries

Vector

A cDNA library was prepared using ptrAP3, a mammalian expression vector containing a cDNA encoding human placental alkaline phosphatase (AP) lacking a signal sequence (FIG. 1 and FIG. 2, SEQ ID NO:1). When ptrAP3 is transfected into a mammalian cell line, such as COS7 cells, AP protein is neither expressed nor secreted since the AP cDNA of ptraAP3 does not encode a translation initiating methionine, a signal peptide, or a membrane anchor sequence. FIG. 3 (SEQ ID NO:2) provides the amino acid sequence of naturally occurring AP. FIG. 4 (SEQ ID NO:3) provides the amino acid sequence of the form of AP encoded by ptrAP3. However, insertion of a cDNA encoding a signal peptide sequence into ptrAP3 such that the signal sequence within the cDNA is fused to and in frame with AP, facilities both the expression and secretion of AP protein upon transfection of the DNA into COS7 cells or other mammalian cells. The presence of AP activity in the supernatants of transfected COS7 cells therefore indicates the presence of a signal sequence in the cDNA of interest.

cDNA Synthesis and Ligation

cDNA for ligation to the ptrAP3 vector was prepared from messenger RNA isolated from human fetal brain tissue (Clontech, Palo Alto, CA: Catalog #6525-1) by a modification of a commercially available "ZAP cDNA synthesis kit" (Stratagene; La Jolla, CA: Catalog # 200401). Synthesis of cDNA involved the following steps.

(a) Single stranded cDNA was synthesized from 5 μg of human fetal brain messenger RNA using a random hexamer primer incorporating a Xhol restriction site (underlined); 5′-CTGACTCGAGNNNNNN-3′ (SEQ ID NO:4). This represented a deviation from the Stratagene protocol and resulted in a population of randomly primed cDNA molecules. Random priming was employed rather than the oligo d(T) priming method suggested by Stratagene in order to generate short cDNA fragments, some of which would be expected to be mRNAs that encode signal sequences.

(b) The single stranded cDNA generated in step (a) was rendered double stranded, and DNA linkers containing a free EcoR1 overhang were ligated to both ends of the double stranded cDNAs using reagents and protocols from the Stratagene ZAP cDNA synthesis kit according to the manufacturer's instructions.

(c) The linker-adapted double-stranded cDNA generated in step (b) was digested with XhoI to generate a free XhoI overhang at the 3′ end of the cDNAs using reagents from the Stratagene ZAP cDNA synthesis kit according to the manufacturers instructions.

(d) Linker-adapted double-stranded cDNAs were size selected by gel filtration through SEPHACRYL™ S-500 cDNA Size Fractionation Columns (Gibco BRL; Bethesda, MD: Catalog #18092-015) according to the manufacturers instructions.

(e) Size selected, double-stranded cDNAs containing a free EcoR1 overhang at the 5′ end and a free XhoI overhang at the 3′ end were ligated to the ptrAP3 backbone which had been digested with EcoR1 and Xhol and purified from the small, released fragment by agarose gel electrophoresis.

(f) Ligated plasmid DNAs were transformed into E. Coli strain DH10b by electroporation.

This process resulted in a library of cDNA clones composed of several million random primed cDNAs (some of which will encode signal sequences) prepared from human fetal brain messenger RNA, fused to the AP reporter cDNA, in the mammalian expression vector ptrAP3.

Step 2 Plating and Automated Picking of Bacterial Colonies

Next, the transformed bacterial cells were plated, and individual clones were identified. A sample of transformed E. coli containing the random primed human fetal brain cDNA library described in Step 1 was plated for growth as individual colonies, using standard procedures. Each E. coli colony contained an individual cDNA clone fused to the AP reporter in the ptrAP3 expression vector. Approximately 20,000 such E. coli colonies were plated, representing approximately 0.5% of the total cDNA library.

Next, E. coli colonies were picked from the plates and inoculated into deep well 96 well plates containing 1 ml of growth medium prepared by standard procedures. Colonies were picked from the plates and E. coli cultures were grown overnight by standard procedures. Each plate was identified by number. Within each plate, each well contained an individual cDNA clone in the ptrAP vector identified by well position.

Finally, plasmid DNA was extracted from the overnight E. coli cultures using a semi-automated 96-well plasmid DNA miniprep procedure, employing standard procedures for bacterial lysis, genomic DNA precipitation and plasmid DNA purification.

The plasmid DNA extraction was performed as follows:

(a) E. coli were centrifuged for 20 minutes using a Beckman Centrifuge at 3200 rpm.

(b) Supernatant was discarded and E. coli pellets were resuspended in 130 µl WP1 (50 mM TRIS (pH 7.5), 10 mM EDTA, 100 µg/ml RNase A) resuspension solution using a TITERTECK MULTIDROP™ apparatus.

(c) E. coli pellets were resuspended by vortexing.

(d) 130 µl WP2 (0.2 M NaOH, 0.5% SDS) lysing solution was added to each well, and the samples were mixed by vortexing for 5 seconds.

(e) 130 µl WP3 (125 mM potassium acetate, pH 4.8) neutralizing solution was added to each well, and the samples were mixed by vortexing for 5 seconds.

(f) Samples were placed on ice for 15 minutes, mixed by vortexing for 5 seconds, and recentrifuged for 10 minutes at 3200 rpm in a Beckman Centrifuge.

(g) Supernatant (crude DNA extract) was transferred from each well of each 96 well plate into a 96 well filter plate (Polyfiltronics) using a TOMTEC/Quadra 96™ transfer apparatus.

(h) 480 µl of Wizard™ Midiprep DNA Purification Resin (Promega) was added to each well of each plate containing crude DNA extract using a Titertek Multidrop apparatus and the samples were left for 5 minutes.

(i) Each 96 well filter plate was placed on a vacuum housing (Polyfiltronics) and the liquid in each well was removed by suction generated by vacuum created with a Lab Port Vacuum pump.

(j) The Wizard Midiprep DNA Purification Resin in each well (to which plasmid DNA was bound) was washed four times with 600 µl of Wizard Wash™.

(k) Plates were centrifuged for 5 minutes to remove excessive moisture from the Wizard Midiprep DNA Purification Resin.

(l) Purified plasmid DNAs were eluted from the Wizard Midiprep DNA Purification Resin into collection plates by addition of 50 µl deionized water to each well

using a Multidrop 8 Channel Pipette, incubation at room temperature for 15 minutes, and centrifugation for 5 minutes (3200 rpm, Beckman centrifuge).

This process resulted in preparation of plasmid DNA contained in 96 well plates with each well containing an individual cDNA clone ligated in the ptrAP expression vector. Individual clones were identified by plate number and well position.

Step 4 Transfection of DNAs into COS7 cells

To determine which of the cDNA clones contained within the cDNA library encoded functional signal peptides, individual plasmid DNA preparations were transfected into COS7 cells as follows.

For each 96 well plate of DNA preparations, one 96 well tissue culture plate containing approximately 10,000 COS7 cells per well was prepared using standard procedures.

Immediately prior to DNA transfection, the COS7 cell culture medium in each well of each 96 well plate was replaced with 80 ul of OptiMEM (Gibco-BRL; catalog #31985-021) containing 1 μl of lipofectamine (Gibco-BRL) and 2 μl (approximately 100-200 ng) of DNA prepared as described above. Thus, each well of each 96 well plate containing COS7 cells received DNA representing one individual cDNA clone from the cDNA library in ptrAP3. The COS7 cells were incubated with the Opti-MEM/Lipofectamine/DNA mixture overnight to allow transfection of cells with the plasmid DNAs.

After overnight incubation, the transfection medium was removed from the cells and replaced with 80 μl fresh medium composed of Opti-MEM + 1% fetal calf serum. Cells were incubated overnight.

Step 5 Alkaline Phosphatase Assay

The secreted alkaline phosphatase activity of the transfected COS7 cells was measured as follows. Samples (10 μl) of supernatants from the transfected COS7 cells were transferred from each well of each 96 well plate into one well of a Microfluor scintillation plate (Dynatech:**Location** Catalog #011-010-7805). AP activity in the supernatants was determined using the Phospha-Light Kit (Tropix Inc.; catalog #BP300). AP assays were performed according to the manufacturer's instruction using a Wallace Micro-Beta scintillation counter.

Step 6 Sequencing and Analysis of Positive Clones

The individual plasmid DNAs scoring positive in the COS7 cell AP secretion assay were analyzed further by DNA sequencing using standard procedures. The resulting DNA sequence information was used to perform BLAST sequence similarity searches of nucleotide protein databases to ascertain whether the clone in question encodes either 1) a known secreted or membrane-associated protein possessing a signal sequence, or 2) a putative novel, secreted or membrane-associated protein possessing a putative novel signal sequence.

Identification of the Protein Tyrosine Phosphatase Sigma (PTPσ) Signal Sequence by Mammalian Signal Peptide trAP

Employing the method described in Example 1, a cDNA clone designated ethb005c07 was found to score positive in the COS7 cell transfection AP assay. BLAST similarity searching with the DNA sequence from this clone identified ethb005c07 as a cDNA encoding the signal sequence of protein tyrosine phosphatase sigma (PTPσ), a previously described protein that is well established in the scientific literature to be a transmembrane protein

(Pulido et al., Proc. Nat'l Acad. Sci. USA 92:11686, 1995).

Identification of a Novel Immunoglobulin Domain Containing Protein by Mammalian Signal Peptide trAP

Employing the method described in Example 1, a cDNA clone designated ethb0018f2 was found to score positive in the COS7 cell transfection AP assay. DNA sequencing revealed that ethb0018f2 harbors a 1455 base pair cDNA having a single open reading frame commencing at nucleotide 55 and continuing to nucleotide 1455. Thus, the ethb0018f2 cDNA encodes a 467 amino acid open reading frame (FIG. 5, SEQ ID NO:5) fused to the AP reporter. Inspection of the ethb0018f2 protein sequence revealed the presence of a putative signal sequence between amino acids 1 to 20, predicted by the signal peptide prediction algorithm, signal P (Von Heijne, Nucleic Acids. Reg. 14:4683-90, 1986). Thus, ethb0018f2 encodes a partial clone of a novel putative secreted/membrane protein. BLAST similarity searching of nucleic acid and protein databases with the ethb0018f2 DNA sequence from this clone revealed similarity to a family of proteins known to contain a protein motif referred to as an Immunoglobulin of IgG domain.

Further visual inspection of the ethb0018f2 protein sequence resulted in the identification of 5 consecutive IgG repeats, defined by a conserved spacing of cysteine, tryptophan, tyrosine, and cysteine residues (FIG. 5).

FIG. 6 is a depiction of a protein sequence alignment between clone ethb0018f2 (referred to as 8f2) and seven related proteins known to contain IgG domains that are also known to be expressed in the brain. These proteins are rat neural adhesion molecule f3 (D38492), Drosophila Neuroglian (P20241), human neural adhesion

molecule L1 (P32004), chick neural adhesion molecule related (P35331), human Axonin 1 (Q02246), rat neural adhesion molecule BIG1 (U11031) and chicken Neurofascin (X65224). Given this sequence similarity, it is likely that clone ethb0018f2 represents a partial cDNA cone representing a novel protein, expressed in the brain, which contains multiple, consecutive IgG domains. Specifically, since the closest relatiaves of clone ethb0018f2 are believed to function as neural adhesion molecules, it is likely that clone ethb0018f2 represents a partial cDNA clone of a novel neural adhesion molecule.

Other Embodiments

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, that the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Millennium Biotherapeutics, Inc.

(ii) TITLE OF THE INVENTION: METHOD FOR IDENTIFYING GENES ENCODING NOVEL SECRETED OR MEMBRANE-ASSOCIATED PROTEIN

(iii) NUMBER OF SEQUENCES: 14

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(B) REGISTRATION NUMBER: 35,283
(C) REFERENCE/DOCKET NUMBER: 09404/020WO1

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617-542-5070
(B) TELEFAX: 617-542-8906
(C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4951 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AAGCTTGGCT GTGGAATGTG TGTCAGTTAG GGTGTGGAAA GTCCCCAGGC TCCCCAGCAG     60
GCAGAAGTAT GCAAAGCATG CATCTCAATT AGTCAGCAAC CAGGTGTGGA AAGTCCCCAG    120
GCTCCCCAGC AGGCAGAAGT ATGCAAAGCA TGCATCTCAA TTAGTCAGCA ACCATAGTCC    180
CGCCCCTAAC TCCGCCCATC CCGCCCCTAA CTCCGCCCAG TTCCGCCCAT TCTCCGCCCC    240
ATGGCTGACT AATTTTTTTT ATTTATGCAG AGGCCGAGGC CGCCTCGGCC TCTGAGCTAT    300
TCCAGAAGTA GTGAGGAGGC TTTTTTGGAG GCCTAGGCTT TTGCAAAAAG CTCCTCCGAT    360
CGAGGGGCTC GCATCTCTCC TTCACGCGCC CGCCGCCCTA CCTGAGGCCG CCATCCACGC    420
CGGTTGAGTC GCGTTCTGCC GCCTCCCGCC TGTGGTGCCT CCTGAACTGC GTCCGCCGTC    480
TAGGTAAGTT TAAAGCTCAG GTCGAGACCG GGCCTTTGTC CGGCGCTCCC TTGGAGCCTA    540
CCTAGACTCA GCCGGCTCTC CACGCTTTGC CTGACCCTGC TTGCTCAACT CTACGTCTTT    600
GTTTCGTTTT CTGTTCTGCG CCGTTACAGA TCCAAGCTCT GAAAAACCAG AAAGTTAACT    660
GGTAAGTTTA GTCTTTTTGT CTTTTATTTC AGGTCCCAGG TCCCGGATCC GGTGATCCAA    720
ATCTAAGAAC TGCTCCTCAG TGAGTGTTGC CTTTACTTCT AGGCCTGTAC GGAAGTGTTA    780
CTTCTGCTCT AAAAGCTGCG GAATTCGCAC CACCGTAGTT TTTACGCCCG GTGAGCGCTC    840
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CACCCGCACC TACAAGCGCG TGTATGATGA GGTGTACGGC GACGAGGACC TGCTTGAGCA   900
GGCCAACGAG CGCCTCGGGG AGTTTGCCTA CGGAAAGCGG CATAAGGACA TGTTGGCGTT   960
GCCGCTGGAC GAGGGCAACC CAACACCTAG CCTAAAGCCC GTGACACTGC AGCAGGTGCT  1020
GCCCACGCTT GCACCGTCCG AAGAAAAGCG CGGCCTAAAG CGCGAGTCTG GTGACTTGGC  1080
ACCCACCGTG CAGCTGATGG TACCCAAGCG CCAGCGACTG GAAGATGTCT TGGAAAAAAT  1140
GACCGTGGAG CCTGGGCTGG AGCCCGAGGT CCGCGTGCGG CCAATCAAGC AGGTGGCACC  1200
GGGACTGGGC GTGCAGACCG TGGACGTTCA GATACCCACC ACCAGTAGCA CTAGTATTGC  1260
CACTGCCACA GAGGGCATGG AGACACAAAC GTCCCCGGTT GCCTAGCTCG AGATCATCCC  1320
AGTTGAGGAG GAGAACCCGG ACTTCTGGAA CCGCGAGGCA GCCGAGGCCC TGGGTGCCGC  1380
CAAGAAGCTG CAGCCTGCAC AGACAGCCGC CAAGAACCTC ATCATCTTCC TGGGCGATGG  1440
GATGGGGGTG TCTACGGTGA CAGCTGCCAG GATCCTAAAA GGGCAGAAGA AGGACAAACT  1500
GGGGCCTGAG ATACCCCTGG CCATGGACCG CTTCCCATAT GTGGCTCTGT CCAAGACATA  1560
CAATGTAGAC AAACATGTGC CAGACAGTGG AGCCACAGCC ACGGCCTACC TGTGCGGGGT  1620
CAAGGGCAAC TTCCAGACCA TTGGCTTGAG TGCAGCCGCC CGCTTTAACC AGTGCAACAC  1680
GACACGCGGC AACGAGGTCA TCTCCGTGAT GAATCGGGCC AAGAAAGCAG GGAAGTCAGT  1740
GGGAGTGGTA ACCACCACAC GAGTGCAGCA CGCCTCGCCA GCCGGCACCT ACGCCCACAC  1800
GGTGAACCGC AACTGGTACT CGGACGCCGA CGTGCCTGCC TCGGCCCGCC AGGAGGGGTG  1860
CCAGGACATC GCTACGCAGC TCATCTCCAA CATGGACATT GACGTGATCC TAGGTGGAGG  1920
CCGAAAGTAC ATGTTTCGCA TGGGAACCCC AGACCCTGAG TACCCAGATG ACTACAGCCA  1980
AGGTGGGACC AGGCTGGACG GGAAGAATCT GGTGCAGGAA TGGCTGGCGA AGCGCCAGGG  2040
TGCCCGGTAT GTGTGGAACC GCACTGAGCT CATGCAGGCT TCCCTGGACC CGTCTGTGAC  2100
CCATCTCATG GGTCTCTTTG AGCCTGGAGA CATGAAATAC GAGATCCACC GAGACTCCAC  2160
ACTGGACCCC TCCCTGATGG AGATGACAGA GGCTGCCCTG CGCCTGCTGA GCAGGAACCC  2220
CCGCGGCTTC TTCCTCTTCG TGGAGGGTGG TCGCATCGAC CATGGTCATC ATGAAAGCAG  2280
GGCTTACCGG GCACTGACTG AGACGATCAT GTTCGACGAC GCCATTGAGA GGGCGGGCCA  2340
GCTCACCAGC GAGGAGGACA CGCTGAGCCT CGTCACTGCC GACCACTCCC ACGTCTTCTC  2400
CTTCGGAGGC TACCCCCTGC GAGGGAGCTC CATCTTCGGG CTGGCCCCTG GCAAGGCCCG  2460
GGACAGGAAG GCCTACACGG TCCTCCTATA CGGAAACGGT CCAGGCTATG TGCTCAAGGA  2520
CGGCGCCCGG CCGGATGTTA CCGAGAGCGA GAGCGGGAGC CCCGAGTATC GGCAGCAGTC  2580
AGCAGTGCCC CTGGACGAAG AGACCCACGC AGGCGAGGAC GTGGCGGTGT TCGCGCGCGG  2640
CCCGCAGGCG CACCTGGTTC ACGGCGTGCA GGAGCAGACC TTCATAGCGC ACGTCATGGC  2700
CTTCGCCGCC TGCCTGGAGC CCTACACCGC CTGCGACCTG GCGCCCCCCG CCGGCACCAC  2760
CGACGCCGCG CACCCGGGTT GAACTAGTCT AGAGAAAAAA CCTCCCACAC CTCCCCCTGA  2820
ACCTGAAACA TAAAATGAAT GCAATTGTTG TTGTTAACTT GTTTATTGCA GCTTATAATG  2880
GTTACAAATA AAGCAATAGC ATCACAAATT TCACAAATAA AGCATTTTTT TCACTGCATT  2940
CTAGTTGTGG TTTGTCCAAA CTCATCAATG TATCTTATCA TGTCTGGATC CCCGGGTACC  3000
GAGCTCGAAT TAATTCCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC TCGGTCGTTC  3060
GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG  3120
GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA  3180
AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCCC TGACGAGCAT CACAAAAATC  3240
GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC  3300
CTGGAAGCTC CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG  3360
CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCAATGCTC ACGCTGTAGG TATCTCAGTT  3420
CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC  3480
GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC  3540
CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG  3600
AGTTCTTGAA GTGGTGGCCT AACTACGGCT ACACTAGAAG GACAGTATTT GGTATCTGCG  3660
CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA  3720
CCACCGCTGG TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAAG  3780
GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT  3840
CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA  3900
ATTAAAAATG AAGTTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT  3960
ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCGT TCATCCATAG  4020
TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA  4080
GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC  4140
AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT  4200
CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG  4260
TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA  4320
GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG  4380
TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA  4440
TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG  4500
TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT  4560
CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA  4620
TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA  4680
GTTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG  4740
TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC  4800
GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT  4860
ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC  4920
CGCGCACATT TCCCCGAAAA GTGCCACCTG C                                  4951
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 530 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Leu Leu Leu Leu Leu Leu Leu Gly Leu Arg Leu Gln Leu Ser Leu
 1               5                  10                  15
Gly Ile Ile Pro Val Glu Glu Glu Asn Pro Asp Phe Trp Asn Arg Glu
            20                  25                  30
Ala Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr
        35                  40                  45
Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser
    50                  55                  60
Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu
65                  70                  75                  80
Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu
                85                  90                  95
Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro Asp Ser Gly Ala Thr
            100                 105                 110
Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly
        115                 120                 125
Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn
    130                 135                 140
Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val
145                 150                 155                 160
Gly Val Val Thr Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Thr
                165                 170                 175
Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro
            180                 185                 190
Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile
        195                 200                 205
Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly Gly Arg Lys Tyr Met
    210                 215                 220
Phe Arg Met Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln
225                 230                 235                 240
Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala
                245                 250                 255
Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln
            260                 265                 270
Ala Ser Leu Asp Pro Ser Val Thr His Leu Met Gly Leu Phe Glu Pro
        275                 280                 285
Gly Asp Met Lys Tyr Glu Ile His Arg Asp Ser Thr Leu Asp Pro Ser
    290                 295                 300
Leu Met Glu Met Thr Glu Ala Ala Leu Arg Leu Leu Ser Arg Asn Pro
305                 310                 315                 320
Arg Gly Phe Phe Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His
                325                 330                 335
His Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu Thr Ile Met Phe Asp
            340                 345                 350
Asp Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser Glu Glu Asp Thr Leu
        355                 360                 365
Ser Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr
    370                 375                 380
Pro Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Arg
385                 390                 395                 400
Asp Arg Lys Ala Tyr Thr Val Leu Leu Tyr Gly Asn Gly Pro Gly Tyr
                405                 410                 415
Val Leu Lys Asp Gly Ala Arg Pro Asp Val Thr Glu Ser Glu Ser Gly
            420                 425                 430
Ser Pro Glu Tyr Arg Gln Gln Ser Ala Val Pro Leu Asp Glu Glu Thr
        435                 440                 445
His Ala Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His
    450                 455                 460
```

```
Leu Val His Gly Val Gln Glu Gln Thr Phe Ile Ala His Val Met Ala
465                 470                 475                 480
Phe Ala Ala Cys Leu Glu Pro Tyr Thr Ala Cys Asp Leu Ala Pro Pro
                485                 490                 495
Ala Gly Thr Thr Asp Ala Ala His Pro Gly Arg Ser Val Val Pro Ala
            500                 505                 510
Leu Leu Pro Leu Leu Ala Gly Thr Leu Leu Leu Leu Glu Thr Ala Thr
        515                 520                 525
Ala Pro
    530
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Ile Ile Pro Val Glu Glu Glu Asn Pro Asp Phe Trp Asn Arg Glu Ala
  1               5                  10                  15
Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu Gln Pro Ala Gln Thr Ala
            20                  25                  30
Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp Gly Met Gly Val Ser Thr
        35                  40                  45
Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Lys Lys Asp Lys Leu Gly
    50                  55                  60
Pro Glu Ile Pro Leu Ala Met Asp Arg Phe Pro Tyr Val Ala Leu Ser
65                  70                  75                  80
Lys Thr Tyr Asn Val Asp Lys His Val Pro Asp Ser Gly Ala Thr Ala
                85                  90                  95
Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Phe Gln Thr Ile Gly Leu
            100                 105                 110
Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn Thr Thr Arg Gly Asn Glu
        115                 120                 125
Val Ile Ser Val Met Asn Arg Ala Lys Lys Ala Gly Lys Ser Val Gly
    130                 135                 140
Val Val Thr Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Thr Tyr
145                 150                 155                 160
Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Val Pro Ala
                165                 170                 175
Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile Ala Thr Gln Leu Ile Ser
            180                 185                 190
Asn Met Asp Ile Asp Val Ile Leu Gly Gly Gly Arg Lys Tyr Met Phe
        195                 200                 205
Arg Met Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Tyr Ser Gln Gly
    210                 215                 220
Gly Thr Arg Leu Asp Gly Lys Asn Leu Val Gln Glu Trp Leu Ala Lys
225                 230                 235                 240
Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg Thr Glu Leu Met Gln Ala
                245                 250                 255
Ser Leu Asp Pro Ser Val Thr His Leu Met Gly Leu Phe Glu Pro Gly
            260                 265                 270
Asp Met Lys Tyr Glu Ile His Arg Asp Ser Thr Leu Asp Pro Ser Leu
        275                 280                 285
Met Glu Met Thr Glu Ala Ala Leu Arg Leu Leu Ser Arg Asn Pro Arg
    290                 295                 300
Gly Phe Phe Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His His
305                 310                 315                 320
Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu Thr Ile Met Phe Asp Asp
                325                 330                 335
Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser Glu Glu Asp Thr Leu Ser
            340                 345                 350
Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr Pro
        355                 360                 365
```

```
Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Arg Asp
    370                 375                 380
Arg Lys Ala Tyr Thr Val Leu Leu Tyr Gly Asn Gly Pro Gly Tyr Val
385                 390                 395                 400
Leu Lys Asp Gly Ala Arg Pro Asp Val Thr Glu Ser Glu Ser Gly Ser
                405                 410                 415
Pro Glu Tyr Arg Gln Gln Ser Ala Val Pro Leu Asp Glu Glu Thr His
            420                 425                 430
Ala Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His Leu
        435                 440                 445
Val His Gly Val Gln Glu Gln Thr Phe Ile Ala His Val Met Ala Phe
    450                 455                 460
Ala Ala Cys Leu Glu Pro Tyr Thr Ala Cys Asp Leu Ala Pro Pro Ala
465                 470                 475                 480
Gly Thr Thr Asp Ala Ala His Pro Gly
                485
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGGACTCGA GNNNNNN 17

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Trp Leu Val Thr Phe Leu Leu Leu Asp Ser Leu His Lys Ala
  1                 5                  10                  15
Arg Pro Glu Asp Val Gly Thr Ser Leu Tyr Phe Val Asn Asp Ser Leu
             20                  25                  30
Gln Gln Val Thr Phe Ser Ser Ser Val Gly Val Val Val Pro Cys Pro
         35                  40                  45
Ala Ala Gly Ser Pro Ser Ala Ala Leu Arg Trp Tyr Leu Ala Thr Gly
     50                  55                  60
Asp Asp Ile Tyr Asp Val Pro His Ile Arg His Val His Ala Asn Gly
 65                  70                  75                  80
Thr Leu Gln Leu Tyr Pro Phe Ser Pro Ser Ala Phe Asn Ser Phe Ile
                 85                  90                  95
His Asp Asn Asp Tyr Phe Cys Thr Ala Glu Asn Ala Ala Gly Lys Ile
            100                 105                 110
Arg Ser Pro Asn Ile Arg Val Lys Ala Val Phe Arg Glu Pro Tyr Thr
        115                 120                 125
Val Arg Val Glu Asp Gln Arg Ser Met Arg Gly Asn Val Ala Val Phe
    130                 135                 140
Lys Cys Leu Ile Pro Ser Ser Val Gln Glu Tyr Val Ser Val Val Ser
145                 150                 155                 160
Trp Glu Lys Asp Thr Val Ser Ile Ile Pro Glu Asn Arg Phe Phe Ile
                165                 170                 175
Thr Tyr His Gly Gly Leu Tyr Ile Ser Asp Val Gln Lys Glu Asp Ala
            180                 185                 190
```

```
Leu Ser Thr Tyr Arg Cys Ile Thr Lys His Lys Tyr Ser Gly Glu Thr
        195                 200                 205
Arg Gln Ser Asn Gly Ala Arg Leu Ser Val Thr Asp Pro Ala Glu Ser
    210                 215                 220
Ile Pro Thr Ile Leu Asp Gly Phe His Ser Gln Glu Val Trp Ala Gly
225                 230                 235                 240
His Thr Val Glu Leu Pro Cys Thr Ala Ser Gly Tyr Pro Ile Pro Ala
                245                 250                 255
Ile Arg Trp Leu Lys Asp Gly Arg Pro Leu Pro Ala Asp Ser Arg Trp
            260                 265                 270
Thr Lys Arg Ile Thr Gly Leu Thr Ile Ser Asp Leu Arg Thr Glu Asp
        275                 280                 285
Ser Gly Thr Tyr Ile Cys Glu Val Thr Asn Thr Phe Gly Ser Ala Glu
    290                 295                 300
Ala Thr Gly Ile Leu Met Val Ile Asp Pro Leu His Val Thr Leu Thr
305                 310                 315                 320
Pro Lys Lys Leu Lys Thr Gly Ile Gly Ser Thr Val Ile Leu Ser Cys
                325                 330                 335
Ala Leu Thr Gly Ser Pro Glu Phe Thr Ile Arg Trp Tyr Arg Asn Thr
            340                 345                 350
Glu Leu Val Leu Pro Asp Glu Ala Ile Ser Ile Arg Gly Leu Ser Asn
        355                 360                 365
Glu Thr Leu Leu Ile Thr Ser Ala Gln Lys Ser His Ser Gly Ala Tyr
    370                 375                 380
Gln Cys Phe Ala Thr Arg Lys Ala Gln Thr Ala Gln Asp Phe Ala Ile
385                 390                 395                 400
Ile Ala Leu Glu Asp Gly Thr Pro Arg Ile Val Ser Ser Phe Ser Glu
                405                 410                 415
Lys Val Val Asn Pro Gly Glu Gln Phe Ser Leu Met Cys Ala Ala Lys
            420                 425                 430
Gly Ala Pro Pro Pro Thr Val Thr Trp Ala Leu Asp Asp Glu Pro Ile
        435                 440                 445
Val Arg Asp Gly Ser His Arg Thr Asn Gln Tyr Thr Met Ser Asp Gly
    450                 455                 460
Thr
465
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: Coding Sequence
(B) LOCATION: 99...1493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
GGCACGAGGG CGGCTGGGAG CGCGCTGAGC GGGGGAGAGG CGCTGCCGCA CGGCCGGCCA     60
CAGGACCACC TCCCCGGAGA ATAGGGCCTC TTTATGGC ATG TGG CTG GTA ACT TTC    116
                                          Met Trp Leu Val Thr Phe
                                            1               5

CTC CTG CTC CTG GAC TCT TTA CAC AAA GCC CGC CCT GAA GAT GTT GGC      164
Leu Leu Leu Leu Asp Ser Leu His Lys Ala Arg Pro Glu Asp Val Gly
             10                  15                  20

ACC AGC CTC TAC TTT GTA AAT GAC TCC TTG CAG CAG GTG ACC TTT TCC      212
Thr Ser Leu Tyr Phe Val Asn Asp Ser Leu Gln Gln Val Thr Phe Ser
         25                  30                  35

AGC TCC GTG GGG GTG GTG GTG CCC TGC CCG GCC GCG GGC TCC CCC AGC      260
Ser Ser Val Gly Val Val Val Pro Cys Pro Ala Ala Gly Ser Pro Ser
     40                  45                  50
```

```
GCG GCC CTT CGA TGG TAC CTG GCC ACA GGG GAC GAC ATC TAC GAC GTG      308
Ala Ala Leu Arg Trp Tyr Leu Ala Thr Gly Asp Asp Ile Tyr Asp Val
 55                  60                  65                  70

CCG CAC ATC CGG CAC GTC CAC GCC AAC GGG ACG CTG CAG CTC TAC CCC      356
Pro His Ile Arg His Val His Ala Asn Gly Thr Leu Gln Leu Tyr Pro
                 75                  80                  85

TTC TCC CCC TCC GCC TTC AAT AGC TTT ATC CAC GAC AAT GAC TAC TTC      404
Phe Ser Pro Ser Ala Phe Asn Ser Phe Ile His Asp Asn Asp Tyr Phe
             90                  95                 100

TGC ACC GCG GAG AAC GCT GCC GGC AAG ATC CGG AGC CCC AAC ATC CGC      452
Cys Thr Ala Glu Asn Ala Ala Gly Lys Ile Arg Ser Pro Asn Ile Arg
        105                 110                 115

GTC AAA GCA GTT TTC AGG GAA CCC TAC ACC GTC CGG GTG GAG GAT CAA      500
Val Lys Ala Val Phe Arg Glu Pro Tyr Thr Val Arg Val Glu Asp Gln
    120                 125                 130

AGG TCA ATG CGT GGC AAC GTG GCC GTC TTC AAG TGC CTC ATC CCC TCT      548
Arg Ser Met Arg Gly Asn Val Ala Val Phe Lys Cys Leu Ile Pro Ser
135                 140                 145                 150

TCA GTG CAG GAA TAT GTT AGC GTT GTA TCT TGG GAG AAA GAC ACA GTC      596
Ser Val Gln Glu Tyr Val Ser Val Val Ser Trp Glu Lys Asp Thr Val
                155                 160                 165

TCC ATC ATC CCA GAA AAC AGG TTT TTT ATT ACC TAC CAC GGC GGG CTG      644
Ser Ile Ile Pro Glu Asn Arg Phe Phe Ile Thr Tyr His Gly Gly Leu
            170                 175                 180

TAC ATC TCT GAC GTA CAG AAG GAG GAC GCC CTC TCC ACC TAT CGC TGC      692
Tyr Ile Ser Asp Val Gln Lys Glu Asp Ala Leu Ser Thr Tyr Arg Cys
        185                 190                 195

ATC ACC AAG CAC AAG TAT AGC GGG GAG ACC CGG CAG AGC AAT GGG GCA      740
Ile Thr Lys His Lys Tyr Ser Gly Glu Thr Arg Gln Ser Asn Gly Ala
    200                 205                 210

CGC CTC TCT GTG ACA GAC CCT GCT GAG TCG ATC CCC ACC ATC CTG GAT      788
Arg Leu Ser Val Thr Asp Pro Ala Glu Ser Ile Pro Thr Ile Leu Asp
215                 220                 225                 230

GGC TTC CAC TCC CAG GAA GTG TGG GCC GGC CAC ACC GTG GAG CTG CCC      836
Gly Phe His Ser Gln Glu Val Trp Ala Gly His Thr Val Glu Leu Pro
                235                 240                 245

TGC ACC GCC TCG GGC TAC CCT ATC CCC GCC ATC CGC TGG CTC AAG GAT      884
Cys Thr Ala Ser Gly Tyr Pro Ile Pro Ala Ile Arg Trp Leu Lys Asp
            250                 255                 260

GGC CGG CCC CTC CCG GCT GAC AGC CGC TGG ACC AAG CGC ATC ACA GGG      932
Gly Arg Pro Leu Pro Ala Asp Ser Arg Trp Thr Lys Arg Ile Thr Gly
        265                 270                 275

CTG ACC ATC AGC GAC TTG CGG ACC GAG GAC AGC GGC ACC TAC ATT TGT      980
Leu Thr Ile Ser Asp Leu Arg Thr Glu Asp Ser Gly Thr Tyr Ile Cys
    280                 285                 290

GAG GTC ACC AAC ACC TTC GGT TCG GCA GAG GCC ACA GGC ATC CTC ATG     1028
Glu Val Thr Asn Thr Phe Gly Ser Ala Glu Ala Thr Gly Ile Leu Met
295                 300                 305                 310

GTC ATT GAT CCC CTT CAT GTG ACC CTG ACA CCA AAG AAG CTG AAG ACC     1076
Val Ile Asp Pro Leu His Val Thr Leu Thr Pro Lys Lys Leu Lys Thr
                315                 320                 325
```

```
GGC ATT GGC AGC ACG GTC ATC CTC TCC TGT GCC CTG ACG GGC TCC CCA     1124
Gly Ile Gly Ser Thr Val Ile Leu Ser Cys Ala Leu Thr Gly Ser Pro
            330                 335                 340

GAG TTC ACC ATC CGC TGG TAT CGC AAC ACG GAG CTG GTG CTG CCT GAC     1172
Glu Phe Thr Ile Arg Trp Tyr Arg Asn Thr Glu Leu Val Leu Pro Asp
        345                 350                 355

GAG GCC ATC TCC ATC CGT GGG CTC AGC AAC GAG ACG CTG CTC ATC ACC     1220
Glu Ala Ile Ser Ile Arg Gly Leu Ser Asn Glu Thr Leu Leu Ile Thr
    360                 365                 370

TCG GCC CAG AAG AGC CAT TCC GGG GCC TAC CAG TGC TTC GCT ACC CGC     1268
Ser Ala Gln Lys Ser His Ser Gly Ala Tyr Gln Cys Phe Ala Thr Arg
375                 380                 385                 390

AAG GCC CAG ACC GCC CAG GAC TTT GCC ATC ATT GCA CTT GAG GAT GGC     1316
Lys Ala Gln Thr Ala Gln Asp Phe Ala Ile Ile Ala Leu Glu Asp Gly
                395                 400                 405

ACG CCC CGC ATC GTC TCG TCC TTC AGC GAG AAG GTG GTC AAC CCC GGG     1364
Thr Pro Arg Ile Val Ser Ser Phe Ser Glu Lys Val Val Asn Pro Gly
            410                 415                 420

GAG CAG TTC TCA CTG ATG TGT GCG GCC AAG GGC GCC CCG CCC CCC ACG     1412
Glu Gln Phe Ser Leu Met Cys Ala Ala Lys Gly Ala Pro Pro Pro Thr
        425                 430                 435

GTC ACC TGG GCC CTC GAC GAT GAG CCC ATC GTG CGG GAT GGC AGC CAC     1460
Val Thr Trp Ala Leu Asp Asp Glu Pro Ile Val Arg Asp Gly Ser His
    440                 445                 450

CGC ACC AAC CAG TAC ACC ATG TCG GAC GGC ACC                         1493
Arg Thr Asn Gln Tyr Thr Met Ser Asp Gly Thr
455                 460                 465
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Met Trp Leu Val Thr Phe Leu Leu Leu Leu Asp Ser Leu His Lys Ala
 1               5                  10                  15
Arg Pro Glu Asp Val Gly Thr Ser Leu Tyr Phe Val Asn Asp Ser Leu
            20                  25                  30
Gln Gln Val Thr Phe Ser Ser Ser Val Gly Val Val Val Pro Cys Pro
        35                  40                  45
Ala Ala Gly Ser Pro Ser Ala Ala Leu Arg Trp Tyr Leu Ala Thr Gly
    50                  55                  60
Asp Asp Ile Tyr Asp Val Pro His Ile Arg His Val His Ala Asn Gly
65                  70                  75                  80
Thr Leu Gln Leu Tyr Pro Phe Ser Pro Ser Ala Phe Asn Ser Phe Ile
                85                  90                  95
His Asp Asn Asp Tyr Phe Cys Thr Ala Glu Asn Ala Ala Gly Lys Ile
            100                 105                 110
Arg Ser Pro Asn Ile Arg Val Lys Ala Val Phe Arg Glu Pro Tyr Thr
        115                 120                 125
Val Arg Val Glu Asp Gln Arg Ser Met Arg Gly Asn Val Ala Val Phe
    130                 135                 140
Lys Cys Leu Ile Pro Ser Ser Val Gln Glu Tyr Val Ser Val Val Ser
145                 150                 155                 160
Trp Glu Lys Asp Thr Val Ser Ile Ile Pro Glu Asn Arg Phe Phe Ile
                165                 170                 175
```

```
Thr Tyr His Gly Gly Leu Tyr Ile Ser Asp Val Gln Lys Glu Asp Ala
            180                 185                 190
Leu Ser Thr Tyr Arg Cys Ile Thr Lys His Lys Tyr Ser Gly Glu Thr
        195                 200                 205
Arg Gln Ser Asn Gly Ala Arg Leu Ser Val Thr Asp Pro Ala Glu Ser
    210                 215                 220
Ile Pro Thr Ile Leu Asp Gly Phe His Ser Gln Glu Val Trp Ala Gly
225                 230                 235                 240
His Thr Val Glu Leu Pro Cys Thr Ala Ser Gly Tyr Pro Ile Pro Ala
                245                 250                 255
Ile Arg Trp Leu Lys Asp Gly Arg Pro Leu Pro Ala Asp Ser Arg Trp
            260                 265                 270
Thr Lys Arg Ile Thr Gly Leu Thr Ile Ser Asp Leu Arg Thr Glu Asp
        275                 280                 285
Ser Gly Thr Tyr Ile Cys Glu Val Thr Asn Thr Phe Gly Ser Ala Glu
    290                 295                 300
Ala Thr Gly Ile Leu Met Val Ile Asp Pro Leu His Val Thr Leu Thr
305                 310                 315                 320
Pro Lys Lys Leu Lys Thr Gly Ile Gly Ser Thr Val Ile Leu Ser Cys
                325                 330                 335
Ala Leu Thr Gly Ser Pro Glu Phe Thr Ile Arg Trp Tyr Arg Asn Thr
            340                 345                 350
Glu Leu Val Leu Pro Asp Glu Ala Ile Ser Ile Arg Gly Leu Ser Asn
        355                 360                 365
Glu Thr Leu Leu Ile Thr Ser Ala Gln Lys Ser His Ser Gly Ala Tyr
    370                 375                 380
Gln Cys Phe Ala Thr Arg Lys Ala Gln Thr Ala Gln Asp Phe Ala Ile
385                 390                 395                 400
Ile Ala Leu Glu Asp Gly Thr Pro Arg Ile Val Ser Ser Phe Ser Glu
                405                 410                 415
Lys Val Val Asn Pro Gly Glu Gln Phe Ser Leu Met Cys Ala Ala Lys
            420                 425                 430
Gly Ala Pro Pro Pro Thr Val Thr Trp Ala Leu Asp Asp Glu Pro Ile
        435                 440                 445
Val Arg Asp Gly Ser His Arg Thr Asn Gln Tyr Thr Met Ser
    450                 455                 460
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 605 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Lys Thr Pro Leu Leu Val Ser His Leu Leu Leu Ile Ser Leu Thr
 1               5                  10                  15
Ser Cys Leu Gly Glu Phe Thr Trp His Arg Arg Tyr Gly His Gly Val
            20                  25                  30
Ser Glu Glu Asp Lys Gly Phe Gly Pro Ile Phe Glu Glu Gln Pro Ile
        35                  40                  45
Asn Thr Ile Tyr Pro Glu Glu Ser Leu Glu Gly Lys Val Ser Leu Asn
    50                  55                  60
Cys Arg Ala Arg Ala Ser Pro Phe Pro Val Tyr Lys Trp Arg Met Asn
65                  70                  75                  80
Asn Gly Asp Val Asp Leu Thr Asn Asp Arg Tyr Ser Met Val Gly Gly
                85                  90                  95
Asn Leu Val Ile Asn Asn Pro Asp Lys Gln Lys Asp Ala Gly Ile Tyr
            100                 105                 110
Tyr Cys Leu Ala Ser Asn Asn Tyr Gly Met Val Arg Ser Thr Glu Ala
        115                 120                 125
Thr Leu Ser Phe Gly Tyr Leu Asp Pro Phe Pro Pro Glu Asp Arg Pro
    130                 135                 140
```

```
Glu Val Lys Val Lys Glu Gly Lys Gly Met Val Leu Leu Cys Asp Pro
145                 150                 155                 160
Pro Tyr His Phe Pro Asp Asp Leu Ser Tyr Arg Trp Leu Leu Asn Glu
                165                 170                 175
Phe Pro Val Phe Ile Thr Met Asp Lys Arg Arg Phe Val Ser Gln Thr
            180                 185                 190
Asn Gly Asn Leu Tyr Ile Ala Asn Val Glu Ser Ser Asp Arg Gly Asn
        195                 200                 205
Tyr Ser Cys Phe Val Ser Ser Pro Ser Ile Thr Lys Ser Val Phe Ser
    210                 215                 220
Lys Phe Ile Pro Leu Ile Pro Ile Pro Glu Arg Thr Thr Lys Pro Tyr
225                 230                 235                 240
Pro Ala Asp Ile Val Val Gln Phe Lys Asp Ile Tyr Thr Met Met Gly
                245                 250                 255
Gln Asn Val Thr Leu Glu Cys Phe Ala Leu Gly Asn Pro Val Pro Asp
            260                 265                 270
Ile Arg Trp Arg Lys Val Leu Glu Pro Met Pro Thr Thr Ala Glu Ile
        275                 280                 285
Ser Thr Ser Gly Ala Val Leu Lys Ile Phe Asn Ile Gln Leu Glu Asp
    290                 295                 300
Glu Gly Leu Tyr Glu Cys Glu Ala Glu Asn Ile Arg Gly Lys Asp Lys
305                 310                 315                 320
His Gln Ala Arg Ile Tyr Val Gln Ala Phe Pro Glu Trp Val Glu His
                325                 330                 335
Ile Asn Asp Thr Glu Val Asp Ile Gly Ser Asp Leu Tyr Trp Pro Cys
            340                 345                 350
Val Ala Thr Gly Lys Pro Ile Pro Thr Ile Arg Trp Leu Lys Asn Gly
        355                 360                 365
Tyr Ala Tyr His Lys Gly Glu Leu Arg Leu Tyr Asp Val Thr Phe Glu
    370                 375                 380
Asn Ala Gly Met Tyr Gln Cys Ile Ala Glu Asn Ala Tyr Gly Thr Ile
385                 390                 395                 400
Tyr Ala Asn Ala Glu Leu Lys Ile Leu Ala Leu Ala Pro Thr Phe Glu
                405                 410                 415
Met Asn Pro Met Lys Lys Lys Ile Leu Ala Ala Lys Gly Gly Arg Val
            420                 425                 430
Ile Ile Glu Cys Lys Pro Lys Ala Ala Pro Lys Pro Lys Phe Ser Trp
        435                 440                 445
Ser Lys Gly Thr Glu Trp Leu Val Asn Ser Ser Arg Ile Leu Ile Trp
    450                 455                 460
Glu Asp Gly Ser Leu Glu Ile Asn Asn Ile Thr Arg Asn Asp Gly Gly
465                 470                 475                 480
Ile Tyr Thr Cys Phe Ala Glu Asn Asn Arg Gly Lys Ala Asn Ser Thr
                485                 490                 495
Gly Thr Leu Val Ile Thr Asn Pro Thr Arg Ile Ile Leu Ala Pro Ile
            500                 505                 510
Asn Ala Asp Ile Thr Val Gly Glu Asn Ala Thr Met Gln Cys Ala Ala
        515                 520                 525
Ser Phe Asp Pro Ser Leu Asp Leu Thr Phe Val Trp Ser Phe Asn Gly
    530                 535                 540
Tyr Val Ile Asp Phe Asn Lys Glu Ile Thr Asn Ile His Tyr Gln Arg
545                 550                 555                 560
Asn Phe Met Leu Asp Ala Asn Gly Glu Leu Leu Ile Arg Asn Ala Gln
                565                 570                 575
Leu Lys His Ala Gly Arg Tyr Thr Cys Thr Ala Gln Thr Ile Val Asp
            580                 585                 590
Asn Ser Ser Ala Ser Ala Asp Leu Val Val Arg Gly Pro
        595                 600                 605
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Met Trp Arg Gln Ser Thr Ile Leu Ala Ala Leu Leu Val Ala Leu Leu
 1               5                  10                  15
Cys Ala Gly Ser Ala Glu Ser Lys Gly Asn Arg Pro Pro Arg Ile Thr
            20                  25                  30
Lys Gln Pro Ala Pro Gly Glu Leu Leu Phe Lys Val Ala Gln Gln Asn
        35                  40                  45
Lys Glu Ser Asp Pro Glu Arg Asn Pro Phe Ile Ile Glu Cys Glu Ala
    50                  55                  60
Asp Gly Gln Pro Glu Pro Glu Tyr Ser Trp Ile Lys Asn Gly Lys Lys
65                  70                  75                  80
Phe Asp Trp Gln Ala Tyr Asp Asn Arg Met Leu Arg Gln Pro Gly Arg
                85                  90                  95
Gly Thr Leu Val Ile Thr Ile Pro Lys Asp Glu Asp Arg Gly His Tyr
            100                 105                 110
Gln Cys Phe Ala Ser Asn Glu Phe Gly Thr Ala Thr Ser Asn Ser Val
        115                 120                 125
Tyr Val Arg Lys Ala Glu Leu Asn Ala Phe Lys Asp Glu Ala Ala Lys
    130                 135                 140
Thr Leu Glu Ala Val Glu Gly Glu Pro Phe Met Leu Lys Cys Ala Ala
145                 150                 155                 160
Pro Asp Gly Phe Pro Ser Pro Thr Val Asn Trp Met Ile Gln Glu Ser
                165                 170                 175
Ile Asp Gly Ser Ile Lys Ser Ile Asn Asn Ser Arg Met Thr Leu Asp
            180                 185                 190
Pro Glu Gly Asn Leu Trp Phe Ser Asn Val Thr Arg Glu Asp Ala Ser
        195                 200                 205
Ser Asp Phe Tyr Tyr Ala Cys Ser Ala Thr Ser Val Phe Arg Ser Glu
    210                 215                 220
Tyr Lys Ile Gly Asn Lys Val Leu Leu Asp Val Lys Gln Met Gly Val
225                 230                 235                 240
Ser Ala Ser Gln Asn Lys His Pro Pro Val Arg Gln Tyr Val Ser Arg
                245                 250                 255
Arg Gln Ser Ala Leu Arg Gly Lys Arg Met Glu Leu Phe Cys Ile Tyr
            260                 265                 270
Gly Gly Thr Pro Leu Pro Gln Thr Val Trp Ser Lys Asp Gly Gln Arg
        275                 280                 285
Ile Gln Trp Ser Asp Arg Ile Thr Gln Gly His Tyr Gly Lys Ser Leu
    290                 295                 300
Val Ile Arg Gln Thr Asn Phe Asp Asp Ala Gly Thr Tyr Thr Cys Asp
305                 310                 315                 320
Val Ser Asn Gly Val Gly Asn Ala Gln Ser Phe Ser Ile Ile Leu Asn
                325                 330                 335
Val Asn Ser Val Pro Tyr Phe Thr Lys Glu Pro Glu Ile Ala Thr Ala
            340                 345                 350
Ala Glu Asp Glu Glu Val Val Phe Glu Cys Arg Ala Ala Gly Val Pro
        355                 360                 365
Glu Pro Lys Ile Ser Trp Ile His Asn Gly Lys Pro Ile Glu Gln Ser
    370                 375                 380
Thr Pro Asn Pro Arg Arg Thr Val Thr Asp Asn Thr Ile Arg Ile Ile
385                 390                 395                 400
Asn Leu Val Lys Gly Asp Thr Gly Asn Tyr Gly Cys Asn Ala Thr Asn
                405                 410                 415
Ser Leu Gly Tyr Val Tyr Lys Asp Val Tyr Leu Asn Val Gln Ala Glu
            420                 425                 430
Pro Pro Thr Ile Ser Glu Ala Pro Ala Ala Val Ser Thr Val Asp Gly
        435                 440                 445
Arg Asn Val Thr Ile Lys Cys Arg Val Asn Gly Ser Pro Lys Pro Leu
    450                 455                 460
Val Lys Trp Leu Arg Ala Ser Asn Trp Leu Thr Gly Gly Arg Tyr Asn
465                 470                 475                 480
Val Gln Ala Asn Gly Asp Leu Glu Ile Gln Asp Val Thr Phe Ser Asp
                485                 490                 495
Ala Gly Lys Tyr Thr Cys Tyr Ala Gln Asn Lys Phe Gly Glu Ile Gln
            500                 505                 510
Ala Asp Gly Ser Leu Val Val Lys Glu His Thr Ile Thr Gln Glu Pro
        515                 520                 525
```

```
Gln Asn Tyr Glu Val Ala Ala Gly Gln Ser Ala Thr Phe Arg Cys Asn
    530                 535                 540
Glu Ala His Asp Asp Thr Leu Glu Ile Glu Ile Asp Trp Trp Lys Asp
545                 550                 555                 560
Gly Gln Ser Ile Asp Phe Glu Ala Gln Pro Arg Phe Val Lys Thr Asn
                565                 570                 575
Asp Asn Ser Leu Thr Ile Ala Lys Thr Met Glu Leu Asp Ser Gly Glu
            580                 585                 590
Tyr Thr Cys Val Ala Arg Thr Arg Leu Asp Glu Ala Thr Ala Arg Ala
        595                 600                 605
Asn Leu Ile Val Gln Asp Val
    610                 615
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 611 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Met Val Val Ala Leu Arg Tyr Val Trp Pro Leu Leu Leu Cys Ser Pro
  1               5                  10                  15
Cys Leu Leu Ile Gln Ile Pro Glu Glu Tyr Glu Gly His His Val Met
            20                  25                  30
Glu Pro Pro Val Ile Thr Glu Gln Ser Pro Arg Arg Leu Val Val Phe
        35                  40                  45
Pro Thr Asp Asp Ile Ser Leu Lys Cys Glu Ala Ser Gly Lys Pro Glu
    50                  55                  60
Val Gln Phe Arg Trp Thr Arg Asp Gly Val His Phe Lys Pro Lys Glu
65                  70                  75                  80
Glu Leu Gly Val Thr Val Tyr Gln Ser Pro His Ser Gly Ser Phe Thr
                85                  90                  95
Ile Thr Gly Asn Asn Ser Asn Phe Ala Gln Arg Phe Gln Gly Ile Tyr
            100                 105                 110
Arg Cys Phe Ala Ser Asn Lys Leu Gly Thr Ala Met Ser His Glu Ile
        115                 120                 125
Arg Leu Met Ala Glu Gly Ala Pro Lys Trp Pro Lys Glu Thr Val Lys
    130                 135                 140
Pro Val Glu Val Glu Glu Gly Glu Ser Val Val Leu Pro Cys Asn Pro
145                 150                 155                 160
Pro Pro Ser Ala Glu Pro Leu Arg Ile Tyr Trp Met Asn Ser Lys Ile
                165                 170                 175
Leu His Ile Lys Gln Asp Glu Arg Val Thr Met Gly Gln Asn Gly Asn
            180                 185                 190
Leu Tyr Phe Ala Asn Val Leu Thr Ser Asp Asn His Ser Asp Tyr Ile
        195                 200                 205
Cys His Ala His Phe Pro Gly Thr Arg Thr Ile Ile Gln Lys Glu Pro
    210                 215                 220
Ile Asp Leu Arg Val Lys Ala Thr Asn Ser Met Ile Asp Arg Lys Pro
225                 230                 235                 240
Arg Leu Leu Phe Pro Thr Asn Ser Ser Ser His Leu Val Ala Leu Gln
                245                 250                 255
Gly Gln Pro Leu Val Leu Glu Cys Ile Ala Glu Gly Phe Pro Thr Pro
            260                 265                 270
Thr Ile Lys Trp Leu Arg Pro Ser Gly Pro Met Pro Ala Asp Arg Val
        275                 280                 285
Thr Tyr Gln Asn His Asn Lys Thr Leu Gln Leu Leu Lys Val Gly Glu
    290                 295                 300
Glu Asp Asp Gly Glu Tyr Arg Cys Leu Ala Glu Asn Ser Leu Gly Ser
305                 310                 315                 320
Ala Arg His Ala Tyr Tyr Val Thr Val Glu Ala Ala Lys Tyr Arg Ile
                325                 330                 335
Gln Arg Gly Ala Leu Ile Leu Ser Asn Val Gln Pro Ser Asp Thr Met
            340                 345                 350
```

```
Val Thr Gln Cys Glu Ala Arg Asn Arg His Gly Leu Leu Leu Ala Asn
        355                 360                 365
Ala Tyr Ile Tyr Val Val Gln Leu Pro Ala Lys Ile Leu Thr Ala Asp
    370                 375                 380
Asn Gln Thr Tyr Met Ala Val Pro Tyr Trp Leu His Lys Pro Gln Ser
385                 390                 395                 400
His Leu Tyr Gly Pro Gly Glu Thr Ala Arg Leu Asp Cys Gln Val Gln
                405                 410                 415
Gly Arg Pro Gln Pro Glu Val Thr Trp Arg Ile Asn Gly Ile Pro Val
            420                 425                 430
Glu Glu Leu Ala Lys Asp Gln Gln Gly Ser Thr Ala Tyr Leu Leu Cys
        435                 440                 445
Lys Ala Phe Gly Ala Pro Val Pro Ser Val Gln Trp Leu Asp Glu Asp
    450                 455                 460
Gly Thr Thr Val Leu Gln Asp Glu Arg Phe Phe Pro Tyr Ala Asn Gly
465                 470                 475                 480
Thr Leu Gly Ile Arg Asp Leu Gln Ala Asn Asp Thr Gly Arg Tyr Phe
                485                 490                 495
Cys Leu Ala Ala Asn Asp Gln Asn Asn Val Thr Ile Met Ala Asn Leu
            500                 505                 510
Lys Val Lys Asp Ala Thr Gln Ile Thr Gln Gly Pro Arg Ser Thr Ile
        515                 520                 525
Glu Lys Lys Gly Ser Arg Val Thr Phe Thr Cys Gln Ala Ser Phe Asp
    530                 535                 540
Pro Ser Leu Gln Pro Ser Ile Thr Trp Arg Gly Asp Gly Arg Asp Leu
545                 550                 555                 560
Gln Glu Leu Gly Asp Ser Asp Lys Tyr Phe Ile Glu Asp Gly Arg Leu
                565                 570                 575
Val Ile His Ser Leu Asp Tyr Ser Asp Gln Gly Asn Tyr Ser Cys Val
            580                 585                 590
Ala Ser Thr Glu Leu Asp Val Val Glu Ser Arg Ala Gln Leu Leu Val
        595                 600                 605
Val Gly Ser
    610
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 612 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
Met Met Lys Glu Lys Ser Ile Ser Ala Ser Lys Ala Ser Leu Val Phe
  1                 5                  10                  15
Phe Leu Cys Gln Met Ile Ser Ala Leu Asp Val Pro Leu Asp Ser Lys
            20                  25                  30
Leu Leu Glu Glu Leu Ser Gln Pro Pro Thr Ile Thr Gln Gln Ser Pro
        35                  40                  45
Lys Asp Tyr Ile Val Asp Pro Arg Glu Asn Ile Val Ile Gln Cys Glu
    50                  55                  60
Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp Thr Arg Asn Gly Thr
65                  70                  75                  80
His Phe Asp Ile Asp Lys Asp Ala Gln Val Thr Met Lys Pro Asn Ser
                85                  90                  95
Gly Thr Leu Val Val Asn Ile Met Asn Gly Val Lys Ala Glu Ala Tyr
            100                 105                 110
Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu Arg Gly Ala Ala Ile
        115                 120                 125
Ser Asn Asn Ile Val Ile Arg Pro Ser Arg Ser Pro Leu Trp Thr Lys
    130                 135                 140
Glu Lys Leu Glu Pro Asn His Val Arg Glu Gly Asp Ser Leu Val Leu
145                 150                 155                 160
Asn Cys Arg Pro Pro Val Gly Leu Pro Pro Pro Ile Ile Phe Trp Met
                165                 170                 175
```

```
Asp Asn Ala Phe Gln Arg Leu Pro Gln Ser Glu Arg Val Ser Gln Gly
            180                 185                 190
Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Gln Pro Glu Asp Thr Arg
        195                 200                 205
Val Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His Thr Gln Thr Ile Gln
    210                 215                 220
Gln Lys Gln Pro Ile Ser Val Lys Val Phe Ser Thr Lys Pro Val Thr
225                 230                 235                 240
Glu Arg Pro Pro Val Leu Leu Thr Pro Met Gly Ser Thr Ser Asn Lys
                245                 250                 255
Val Glu Leu Arg Gly Asn Val Leu Leu Leu Glu Cys Ile Ala Ala Gly
            260                 265                 270
Leu Pro Thr Pro Val Ile Arg Trp Ile Lys Glu Gly Gly Glu Leu Pro
        275                 280                 285
Ala Asn Arg Thr Phe Phe Glu Asn Phe Lys Lys Thr Leu Lys Ile Ile
    290                 295                 300
Asp Val Ser Glu Ala Asp Ser Gly Asn Tyr Lys Cys Thr Ala Arg Asn
305                 310                 315                 320
Thr Leu Gly Ser Thr His His Val Ile Ser Val Thr Val Lys Ala Ala
                325                 330                 335
Pro Tyr Trp Ile Thr Ala Pro Arg Asn Leu Val Leu Ser Pro Gly Glu
            340                 345                 350
Asp Gly Thr Leu Ile Cys Arg Ala Asn Gly Asn Pro Lys Pro Ser Ile
        355                 360                 365
Ser Trp Leu Thr Asn Gly Val Pro Ile Ala Ile Ala Pro Glu Asp Pro
    370                 375                 380
Ser Arg Lys Val Asp Gly Asp Thr Ile Ile Phe Ser Ala Val Gln Glu
385                 390                 395                 400
Arg Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser Asn Glu Tyr Gly Tyr
                405                 410                 415
Leu Leu Ala Asn Ala Phe Val Asn Val Leu Ala Glu Pro Pro Arg Ile
            420                 425                 430
Leu Thr Pro Ala Asn Lys Leu Tyr Gln Val Ile Ala Asp Ser Pro Ala
        435                 440                 445
Leu Ile Asp Cys Ala Tyr Phe Gly Ser Pro Lys Pro Glu Ile Glu Trp
    450                 455                 460
Phe Arg Gly Val Lys Gly Ser Ile Leu Arg Gly Asn Glu Tyr Val Phe
465                 470                 475                 480
His Asp Asn Gly Thr Leu Glu Ile Pro Val Ala Gln Lys Asp Ser Thr
                485                 490                 495
Gly Thr Tyr Thr Cys Val Ala Arg Asn Lys Leu Gly Lys Thr Gln Asn
            500                 505                 510
Glu Val Gln Leu Glu Val Lys Asp Pro Thr Met Ile Ile Lys Gln Pro
        515                 520                 525
Gln Tyr Lys Val Ile Gln Arg Ser Ala Gln Ala Ser Phe Glu Cys Val
    530                 535                 540
Ile Lys His Asp Pro Thr Leu Ile Pro Thr Val Ile Trp Leu Lys Asp
545                 550                 555                 560
Asn Asn Glu Leu Pro Asp Asp Glu Arg Phe Leu Val Gly Lys Asp Asn
                565                 570                 575
Leu Thr Ile Met Asn Val Thr Asp Lys Asp Asp Gly Thr Tyr Thr Cys
            580                 585                 590
Ile Val Asn Thr Thr Leu Asp Ser Val Ser Ala Ser Ala Val Leu Thr
        595                 600                 605
Val Val Ala Ala
    610
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 607 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Thr Ala Thr Arg Arg Lys Pro His Leu Leu Leu Val Ala Ala
1 5 10 15
Val Ala Leu Val Ser Ser Ser Ala Trp Ser Ser Ala Leu Gly Ser Gln
20 25 30
Thr Thr Phe Gly Pro Val Phe Glu Asp Gln Pro Leu Ser Val Leu Phe
35 40 45
Pro Glu Glu Ser Thr Glu Glu Gln Val Leu Leu Ala Cys Arg Ala Arg
50 55 60
Ala Ser Pro Pro Ala Thr Tyr Arg Trp Lys Met Asn Gly Thr Glu Met
65 70 75 80
Lys Leu Glu Pro Gly Ser Arg His Gln Leu Val Gly Gly Asn Leu Val
85 90 95
Ile Met Asn Pro Thr Lys Ala Gln Asp Ala Gly Val Tyr Gln Cys Leu
100 105 110
Ala Ser Asn Pro Val Gly Thr Val Val Ser Arg Glu Ala Ile Leu Arg
115 120 125
Phe Gly Phe Leu Gln Glu Phe Ser Lys Glu Glu Arg Asp Pro Val Lys
130 135 140
Ala His Glu Gly Trp Gly Val Met Leu Pro Cys Asn Pro Pro Ala His
145 150 155 160
Tyr Pro Gly Leu Ser Tyr Arg Trp Leu Leu Asn Glu Phe Pro Asn Phe
165 170 175
Ile Pro Thr Asp Gly Arg His Phe Val Ser Gln Thr Thr Gly Asn Leu
180 185 190
Tyr Ile Ala Arg Thr Asn Ala Ser Asp Leu Gly Asn Tyr Ser Cys Leu
195 200 205
Ala Thr Ser His Met Asp Phe Ser Thr Lys Ser Val Phe Ser Lys Phe
210 215 220
Ala Gln Leu Asn Leu Ala Ala Glu Asp Thr Arg Leu Phe Ala Pro Ser
225 230 235 240
Ile Lys Ala Arg Phe Pro Ala Glu Thr Tyr Ala Leu Val Gly Gln Gln
245 250 255
Val Thr Leu Glu Cys Phe Ala Phe Gly Asn Pro Val Pro Arg Ile Lys
260 265 270
Trp Arg Lys Val Asp Gly Ser Leu Ser Pro Gln Trp Thr Thr Ala Glu
275 280 285
Pro Thr Leu Gln Ile Pro Ser Val Ser Phe Glu Asp Glu Gly Thr Tyr
290 295 300
Glu Cys Glu Ala Glu Asn Ser Lys Gly Arg Asp Thr Val Gln Gly Arg
305 310 315 320
Ile Ile Val Gln Ala Gln Pro Glu Trp Leu Lys Val Ile Ser Asp Thr
325 330 335
Glu Ala Asp Ile Gly Ser Asn Leu Arg Trp Gly Cys Ala Ala Ala Gly
340 345 350
Lys Pro Arg Pro Thr Val Arg Trp Leu Arg Asn Gly Glu Pro Leu Ala
355 360 365
Ser Gln Asn Arg Val Glu Val Leu Ala Gly Asp Leu Arg Phe Ser Lys
370 375 380
Leu Ser Leu Glu Asp Ser Gly Met Tyr Gln Cys Val Ala Glu Asn Lys
385 390 395 400
His Gly Thr Ile Tyr Ala Ser Ala Glu Leu Ala Val Gln Ala Leu Ala
405 410 415
Pro Asp Phe Arg Leu Asn Pro Val Arg Arg Leu Ile Pro Ala Ala Arg
420 425 430
Gly Gly Glu Ile Leu Ile Pro Cys Gln Pro Arg Ala Ala Pro Lys Ala
435 440 445
Val Val Leu Trp Ser Lys Gly Thr Glu Ile Leu Val Asn Ser Ser Arg
450 455 460
Val Thr Val Thr Pro Asp Gly Thr Leu Ile Ile Arg Asn Ile Ser Arg
465 470 475 480
Ser Asp Glu Gly Lys Tyr Thr Cys Phe Ala Glu Asn Phe Met Gly Lys
485 490 495
Ala Asn Ser Thr Gly Ile Leu Ser Val Arg Asp Ala Thr Lys Ile Thr
500 505 510
Leu Ala Pro Ser Ser Ala Asp Ile Asn Leu Gly Asp Asn Leu Thr Leu
515 520 525

```
Gln Cys His Ala Ser His Asp Pro Thr Met Asp Leu Thr Phe Thr Trp
    530                 535                 540
Thr Leu Asp Asp Phe Pro Ile Asp Phe Asp Lys Pro Gly Gly His Tyr
545                 550                 555                 560
Arg Arg Thr Asn Val Lys Glu Thr Ile Gly Asp Leu Thr Ile Leu Asn
                565                 570                 575
Ala Gln Leu Arg His Gly Gly Lys Tyr Thr Cys Met Ala Gln Thr Val
            580                 585                 590
Val Asp Ser Ala Ser Lys Glu Ala Thr Val Leu Val Arg Gly Pro
        595                 600                 605
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 596 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Met Leu Ser Trp Lys Gln Leu Ile Leu Leu Ser Phe Ile Gly Cys Leu
  1                 5                  10                  15
Ala Gly Glu Leu Leu Leu Gln Gly Pro Val Phe Val Lys Glu Pro Ser
            20                  25                  30
Asn Ser Ile Phe Pro Val Gly Ser Glu Asp Lys Lys Ile Thr Leu Asn
        35                  40                  45
Cys Glu Ala Arg Gly Asn Pro Ser Pro His Tyr Arg Trp Gln Leu Asn
    50                  55                  60
Gly Ser Asp Ile Asp Thr Ser Leu Asp His Arg Tyr Lys Leu Asn Gly
65                  70                  75                  80
Gly Asn Leu Ile Val Ile Asn Pro Asn Arg Asn Trp Asp Thr Gly Ser
                85                  90                  95
Tyr Gln Cys Phe Ala Thr Asn Ser Leu Gly Thr Ile Val Ser Arg Glu
            100                 105                 110
Ala Lys Leu Gln Phe Ala Tyr Leu Glu Asn Phe Lys Ser Arg Met Arg
        115                 120                 125
Ser Arg Val Ser Val Arg Glu Gly Gln Gly Val Val Leu Leu Cys Gly
    130                 135                 140
Pro Pro Pro His Ser Gly Glu Leu Ser Tyr Ala Trp Val Phe Asn Glu
145                 150                 155                 160
Tyr Pro Ser Phe Val Glu Glu Asp Ser Arg Arg Phe Val Ser Gln Glu
                165                 170                 175
Thr Gly His Leu Tyr Ile Ala Lys Val Glu Pro Ser Asp Val Gly Asn
            180                 185                 190
Tyr Thr Cys Val Val Thr Ser Thr Val Thr Asn Ala Arg Val Leu Gly
        195                 200                 205
Ser Pro Thr Pro Leu Val Leu Arg Ser Asp Gly Val Met Gly Glu Tyr
    210                 215                 220
Glu Pro Lys Ile Glu Leu Gln Phe Pro Glu Thr Leu Pro Ala Ala Lys
225                 230                 235                 240
Gly Ser Thr Val Lys Leu Glu Cys Phe Ala Leu Gly Asn Pro Val Pro
                245                 250                 255
Gln Ile Asn Trp Arg Arg Ser Asp Gly Met Pro Phe Pro Thr Lys Ile
            260                 265                 270
Lys Leu Arg Lys Phe Asn Gly Val Leu Glu Ile Pro Asn Phe Gln Gln
        275                 280                 285
Glu Asp Thr Gly Ser Tyr Glu Cys Ile Ala Glu Asn Ser Arg Gly Lys
    290                 295                 300
Asn Val Ala Arg Gly Arg Leu Thr Tyr Tyr Ala Lys Pro Tyr Trp Val
305                 310                 315                 320
Gln Leu Leu Lys Asp Val Glu Thr Ala Val Glu Asp Ser Leu Tyr Trp
                325                 330                 335
Glu Cys Arg Ala Ser Gly Lys Pro Lys Pro Ser Tyr Arg Trp Leu Lys
            340                 345                 350
Asn Gly Asp Ala Leu Val Leu Glu Glu Arg Ile Gln Ile Glu Asn Gly
        355                 360                 365
```

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Ala Leu Thr Ile Ala Asn Leu Asn Val Ser Asp Ser Gly Met Phe Gln
    370                 375                 380
Cys Ile Ala Glu Asn Lys His Gly Leu Ile Tyr Ser Ser Ala Glu Leu
385                 390                 395                 400
Lys Val Leu Ala Ser Ala Pro Asp Phe Ser Arg Asn Pro Met Lys Lys
                405                 410                 415
Met Ile Gln Val Gln Val Gly Ser Leu Val Ile Leu Asp Cys Lys Pro
            420                 425                 430
Ser Ala Ser Pro Arg Ala Leu Ser Phe Trp Lys Lys Gly Asp Thr Val
        435                 440                 445
Val Arg Glu Gln Ala Arg Ile Ser Leu Leu Asn Asp Gly Gly Leu Lys
    450                 455                 460
Ile Met Asn Val Thr Lys Ala Asp Ala Gly Ile Tyr Thr Cys Ile Ala
465                 470                 475                 480
Glu Asn Gln Phe Gly Lys Ala Asn Gly Thr Thr Gln Leu Val Val Thr
                485                 490                 495
Glu Pro Thr Arg Ile Ile Leu Ala Pro Ser Asn Met Asp Val Ala Val
            500                 505                 510
Gly Glu Ser Ile Ile Leu Pro Cys Gln Val Gln His Asp Pro Leu Leu
        515                 520                 525
Asp Ile Met Phe Ala Trp Tyr Phe Asn Gly Thr Leu Thr Asp Phe Lys
    530                 535                 540
Lys Asp Gly Ser His Phe Glu Lys Val Gly Gly Ser Ser Ser Gly Asp
545                 550                 555                 560
Leu Met Ile Arg Asn Ile Gln Leu Lys His Ser Gly Lys Tyr Val Cys
                565                 570                 575
Met Val Gln Thr Gly Val Asp Ser Val Ser Ser Ala Ala Glu Leu Ile
            580                 585                 590
Val Arg Gly Ser
        595
```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 630 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Val Leu His Ser His Gln Leu Thr Tyr Ala Gly Ile Ala Phe Ala
  1                 5                  10                  15
Leu Cys Leu His His Leu Ile Ser Ala Ile Glu Val Pro Leu Asp Ser
            20                  25                  30
Asn Ile Gln Ser Glu Leu Pro Gln Pro Pro Thr Ile Thr Lys Gln Ser
        35                  40                  45
Val Lys Asp Tyr Ile Val Asp Pro Arg Asp Asn Ile Phe Ile Glu Cys
    50                  55                  60
Glu Ala Lys Gly Asn Pro Val Pro Thr Phe Ser Trp Thr Arg Asn Gly
65                  70                  75                  80
Lys Phe Phe Asn Val Ala Lys Asp Pro Lys Val Ser Met Arg Arg Arg
                85                  90                  95
Ser Gly Thr Leu Val Ile Asp Phe His Gly Gly Gly Arg Pro Asp Asp
            100                 105                 110
Tyr Glu Gly Glu Tyr Gln Cys Phe Ala Arg Asn Asp Tyr Gly Thr Ala
        115                 120                 125
Leu Ser Ser Lys Ile His Leu Gln Val Ser Arg Ser Pro Leu Trp Pro
    130                 135                 140
Lys Glu Lys Val Asp Val Ile Glu Val Asp Glu Gly Ala Pro Leu Ser
145                 150                 155                 160
Leu Gln Cys Asn Pro Pro Pro Gly Leu Pro Pro Pro Val Ile Phe Trp
                165                 170                 175
Met Ser Ser Ser Met Glu Pro Ile His Gln Asp Lys Arg Val Ser Gln
            180                 185                 190
Gly Gln Asn Gly Asp Leu Tyr Phe Ser Asn Val Met Leu Gln Asp Ala
        195                 200                 205
```

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Gln Thr Asp Tyr Ser Cys Asn Ala Arg Phe His Phe Thr His Thr Ile
    210                 215                 220
Gln Gln Lys Asn Pro Tyr Thr Leu Lys Val Lys Thr Lys Lys Pro His
225                 230                 235                 240
Asn Glu Thr Ser Leu Arg Asn His Thr Asp Met Tyr Ser Ala Arg Gly
                245                 250                 255
Val Thr Glu Thr Thr Pro Ser Phe Met Tyr Pro Tyr Gly Thr Ser Ser
            260                 265                 270
Ser Gln Met Val Leu Arg Gly Val Asp Leu Leu Leu Glu Cys Ile Ala
        275                 280                 285
Ser Gly Val Pro Ala Pro Asp Ile Met Trp Tyr Lys Lys Gly Gly Glu
    290                 295                 300
Leu Pro Ala Gly Lys Thr Lys Leu Glu Asn Phe Asn Lys Ala Leu Arg
305                 310                 315                 320
Ile Ser Asn Val Ser Glu Glu Asp Ser Gly Glu Tyr Phe Cys Leu Ala
                325                 330                 335
Ser Asn Lys Met Gly Ser Ile Arg His Thr Ile Ser Val Arg Val Lys
            340                 345                 350
Ala Ala Pro Tyr Trp Leu Asp Glu Pro Gln Asn Leu Ile Leu Ala Pro
        355                 360                 365
Gly Glu Asp Gly Arg Leu Val Cys Arg Ala Asn Gly Asn Pro Lys Pro
    370                 375                 380
Ser Ile Gln Trp Leu Val Asn Gly Glu Pro Ile Glu Gly Ser Pro Pro
385                 390                 395                 400
Asn Pro Ser Arg Glu Val Ala Gly Asp Thr Ile Val Phe Arg Asp Thr
                405                 410                 415
Gln Ile Gly Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser Asn Glu His
            420                 425                 430
Gly Tyr Leu Leu Ala Asn Ala Phe Val Ser Val Leu Asp Val Pro Pro
        435                 440                 445
Arg Ile Leu Ala Pro Arg Asn Gln Leu Ile Lys Val Ile Gln Tyr Asn
    450                 455                 460
Arg Thr Arg Leu Asp Cys Pro Phe Phe Gly Ser Pro Ile Pro Thr Leu
465                 470                 475                 480
Arg Trp Phe Lys Asn Gly Gln Gly Asn Met Leu Asp Gly Gly Asn Tyr
                485                 490                 495
Lys Ala His Glu Asn Gly Ser Leu Glu Met Ser Met Ala Arg Lys Glu
            500                 505                 510
Asp Gln Gly Ile Tyr Thr Cys Val Ala Thr Asn Ile Leu Gly Lys Val
        515                 520                 525
Glu Ala Gln Val Arg Leu Glu Val Lys Asp Pro Thr Arg Ile Val Arg
    530                 535                 540
Gly Pro Glu Asp Gln Val Val Lys Arg Gly Ser Met Pro Arg Leu His
545                 550                 555                 560
Cys Arg Val Lys His Asp Pro Thr Leu Lys Leu Thr Val Thr Trp Leu
                565                 570                 575
Lys Asp Asp Ala Pro Leu Tyr Ile Gly Asn Arg Met Lys Lys Glu Asp
            580                 585                 590
Asp Gly Leu Thr Ile Tyr Gly Val Ala Glu Lys Asp Gln Gly Asp Tyr
        595                 600                 605
Thr Cys Val Ala Ser Thr Glu Leu Asp Lys Asp Ser Ala Lys Ala Tyr
    610                 615                 620
Leu Thr Val Leu Ala Ile
625                 630
```

What is claimed is:

1. A method for identifying a cDNA nucleic acid encoding a mammalian protein having a signal sequence, the method comprising:

a) providing library of mammalian cDNA;

b) ligating said library of mammalian cDNA to DNA encoding alkaline phosphatase lacking both a signal sequence and a membrane anchor sequence to form ligated DNA;

c) transforming bacterial cells with said ligated DNA to create a bacterial cell clone library;

d) isolating DNA comprising said mammalian cDNA from at least one clone in said bacterial cell clone library;

e) separately transfecting DNA isolated from clones in step (d) into mammalian cells which do not express alkaline phosphatase to create a mammalian cell clone library wherein each clone in said mammalian cell clone library corresponds to a clone in said bacterial cell clone library;

f) identifying a clone in said mammalian cell clone library which express alkaline phosphatase;

g) identifying the clone in said bacterial cell clone library corresponding to said clone in said mammalian cell clone library identified in step (f); and

h) isolating and sequencing a portion of the mammalian cDNA present in said bacterial cell library clone identified in step (g) to identify a mammalian cDNA encoding a mammalian protein having a signal sequence.

2. The method of claim 1 wherein said library of mammalian cDNAs are ligated to ptrAP3.

3. The method of claim 1 wherein said mammalian cells are COS7 cells.

4. The method of claim 1 wherein said bacterial cells are E. coli.

5. The expression vector ptrAP3.

6. The expression vector of claim 5, comprising the sequence of SEQ ID NO:1.

7. The protein of SEQ ID NO:5.

8. An isolated nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:5.

9. A vector comprising the nucleic acid sequence of claim 8.

10. The vector of claim 9 wherein said vector is an expression vector.

11. A genetically engineered host cell comprising the nucleic acid sequence of claim 5.

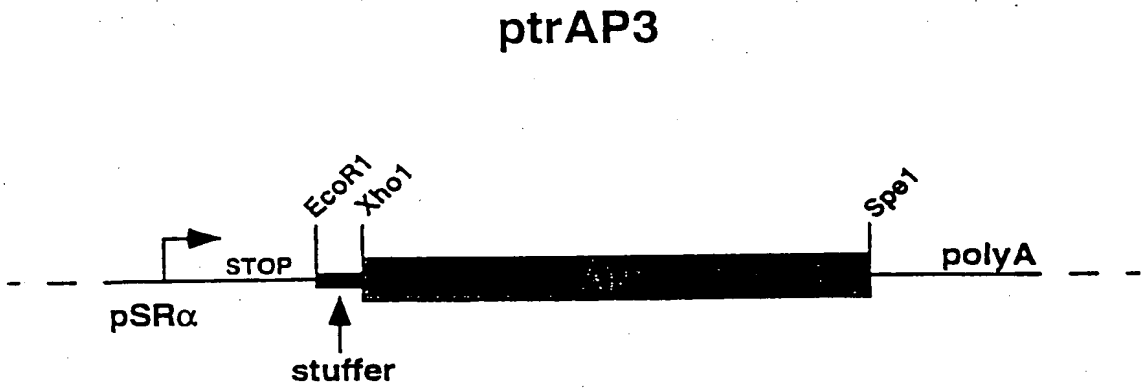

FIG. 1

ptrAP3 vector sequence

AAGCTTGGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGC

AAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGC

AAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGC

CCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGG

CCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTCCTCCGAT

CGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCCGCCATCCACGCCGGTTGAGTCGC

GTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCG

AGACCGGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACC

CTGCTTGCTCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTCTGAAAAACC

AGAAAGTTAACTGGTAAGTTTAGTCTTTTTGTCTTTTATTTCAGGTCCCAGGTCCCGGATCCGGTGATCCAA

ATCTAAGAACTGCTCCTCAGTGAGTGTTGCCTTTACTTCTAGGCCTGTACGGAAGTGTTACTTCTGCTCTAA

AAGCTGCG**GAATTCGCACCACCGTAGTTTTTACGCCCGGTGAGCGCTCCACCCGCACCTACA**

AGCGCGTGTATGATGAGGTGTACGGCGACGAGGACCTGCTTGAGCAGGCCAACGAGCGCCT

CGGGGAGTTTGCCTACGGAAAGCGGCATAAGGACATGTTGGCGTTGCCGCTGGACGAGGGC

AAGCCAACACCTAGCCTAAAGCCCGTGACACTGCAGCAGGTGCTGCCCACGCTTGCACCGT

CCGAAGAAAAGCGCGGCCTAAAGCGCGAGTCTGGTGACTTGGCACCCACCGTGCAGCTGAT

GGTACCCAAGCGCCAGCGACTGGAAGATGTCTTGGAAAAAATGACCGTGGAGCCTGGGCTG

GAGCCCGAGGTCCGCGTGCGGCCAATCAAGCAGGTGGCACCGGGACTGGGCGTGCAGACCG

TGGACGTTCAGATACCCACCACCAGTAGCACTAGTATTGCCACTGCCACAGAGGGCATGGA

GACACAAACGTCCCCGGTTGCCTAGCTCGAGATCATCCCAGTTGAGGAGGAGAACCCGGACTTCTG

GAACCGCGAGGCAGCCGAGGCCCTGGGTGCCGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCT

CATCATCTTCCTGGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCCTAAAAGGGCAGAAGAA

GGACAAACTGGGGCCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGCTCTGTCCAAGACATACAA

TGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGGCCTACCTGTGCGGGGTCAAGGGCAACTTCCA

GACCATTGGCTTGAGTGCAGCCGCCCGCTTTAACCAGTGCAACACGACACGCGGCAACGAGGTCATCTCCGT

GATGAATCGGGCCAAGAAAGCAGGGAAGTCAGTGGGAGTGGTAACCACCACACGAGTGCAGCACGCCTCGCC

AGCCGGCACCTACGCCCACACGGTGAACCGCAACTGGTACTCGGACGCCGACGTGCCTGCCTCGGCCCGCCA

GGAGGGGTGCCAGGACATCGCTACGCAGCTCATCTCCAACATGGACATTGACGTGATCCTAGGTGGAGGCCG

FIG. 2

AAAGTACATGTTTCGCATGGGAACCCCAGACCCTGAGTACCCAGATGACTACAGCCAAGGTGGGACCAGGCT
GGACGGGAAGAATCTGGTGCAGGAATGGCTGGCGAAGCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGA
GCTCATGCAGGCTTCCCTGGACCCGTCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGAAATA
CGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGACAGAGGCTGCCCTGCGCCTGCTGAG
CAGGAACCCCCGCGGCTTCTTCCTCTTCGTGGAGGGTGGTCGCATCGACCATGGTCATCATGAAAGCAGGGC
TTACCGGGCACTGACTGAGACGATCATGTTCGACGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGA
GGACACGCTGAGCCTCGTCACTGCCGACCACTCCCACGTCTTCTCCTTCGGAGGCTACCCCCTGCGAGGGAG
CTCCATCTTCGGGCTGGCCCCTGGCAAGGCCCGGGACAGGAAGGCCTACACGGTCCTCCTATACGGAAACGG
TCCAGGCTATGTGCTCAAGGACGGCGCCCGGCCGGATGTTACCGAGAGCGAGAGCGGGAGCCCCGAGTATCG
GCAGCAGTCAGCAGTGCCCCTGGACGAAGAGACCCACGCAGGCGAGGACGTGGCGGTGTTCGCGCGCGGCCC
GCAGGCGCACCTGGTTCACGGCGTGCAGGAGCAGACCTTCATAGCGCACGTCATGGCCTTCGCCGCCTGCCT
GGAGCCCTACACCGCCTGCGACCTGGCGCCCCCCGCCGGCACCACCGACGCCGCGCACCCGGGTTGAACTAG
TCTAGAGAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACT
TGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTT
CACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGATCCCCGGGTACCGAG
CTCGAATTAATTCCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGG
TATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG
CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC
CTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG
CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCT
TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTC
GCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC
TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGA
GGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTG
GTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCA
CCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATC
CTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT
TATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATG
AGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTT
CATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTG
CTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGG
CCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAG
TAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGT
CGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCA
AAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGG

FIG. 2

TTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACT
CAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATA
CCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGA
TCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTT
TCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGA
AATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCG
GATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCAC
CTGC (SEQ ID NO: 1)

FIG. 2

FIG. 3

MLLLLLLLLGLRLQLSLGIIPVEEENPDFWNREAAEALGAAKKLQPAQTAAKNLI
IFLGDGMGVSTVTAARILKGQKKDKLGPEIPLAMDRFPYVALSKTYNVDKHVPD
SGATATAYLCGVKGNFQTIGLSAAARFNQCNTTRGNEVISVMNRAKKAGKSVGV
VTTTRVQHASPAGTYAHTVNRNWYSDADVPASARQEGCQDIATQLISNMDIDVI
LGGGRKYMFRMGTPDPEYPDDYSQGGTRLDGKNLVQEWLAKRQGARYVWNRTEL
MQASLDPSVTHLMGLFEPGDMKYEIHRDSTLDPSLMEMTEAALRLLSRNPRGFF
LFVEGGRIDHGHHESRAYRALTETIMFDDAIERAGQLTSEEDTLSLVTADHSHV
FSFGGYPLRGSSIFGLAPGKARDRKAYTVLLYGNGPGYVLKDGARPDVTESESG
SPEYRQQSAVPLDEETHAGEDVAVFARGPQAHLVHGVQEQTFIAHVMAFAACLE
PYTACDLAPPAGTTDAAHPG**RSVVPALLPLLAGTLLLLETATAP**

(SEQ ID NO:2)

FIG. 4

IIPVEEENPDFWNREAAEALGAAKKLQPAQTAAKNLIIFLGDGMGVSTVTAARI
LKGQKKDKLGPEIPLAMDRFPYVALSKTYNVDKHVPDSGATATAYLCGVKGNFQ
TIGLSAAARFNQCNTTRGNEVISVMNRAKKAGKSVGVVTTTRVQHASPAGTYAH
TVNRNWYSDADVPASARQEGCQDIATQLISNMDIDVILGGGRKYMFRMGTPDPE
YPDDYSQGGTRLDGKNLVQEWLAKRQGARYVWNRTELMQASLDPSVTHLMGLFE
PGDMKYEIHRDSTLDPSLMEMTEAALRLLSRNPRGFFLFVEGGRIDHGHHESRA
YRALTETIMFDDAIERAGQLTSEEDTLSLVTADHSHVFSFGGYPLRGSSIFGLA
PGKARDRKAYTVLLYGNGPGYVLKDGARPDVTESESGSPEYRQQSAVPLDEETH
AGEDVAVFARGPQAHLVHGVQEQTFIAHVMAFAACLEPYTACDLAPPAGTTDAA
HPG

(SEQ ID NO:3)

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GGCACGAGGGCGGCTGGGAGCGCGCTGAGCGGGGGAGAGGCGCTGCCGCACGGCCGGCCACAGGACCACCTCCCCCGGAG  79

                          M   W   L   V   T   F   L   L   L   L   D   S   L   H   K    15
AATAGGGCCTCTTTATGGC ATG TGG CTG GTA ACT TTC CTC CTG CTC CTG GAC TCT TTA CAC AAA  143

 A   R   P   E   D   V   G   T   S   L   Y   F   V   N   D   S   L   Q   Q   V    35
GCC CGC CCT GAA GAT GTT GGC ACC AGC CTC TAC TTT GTA AAT GAC TCC TTG CAG CAG GTG  203

 T   F   S   S   S   V   G   V   V   V   P   C   P   A   A   G   S   P   S   A    55
ACC TTT TCC AGC TCC GTG GGG GTG GTG GTG CCC TGC CCG GCC GCG GGC TCC CCC AGC GCG  263

 A   L   R   W   Y   L   A   T   G   D   D   I   Y   D   V   P   H   I   R   H    75
GCC CTT CGA TGG TAC CTG GCC ACA GGG GAC GAC ATC TAC GAC GTG CCG CAC ATC CGG CAC  323

 V   H   A   N   G   T   L   Q   L   Y   P   F   S   P   S   A   F   N   S   F    95
GTC CAC GCC AAC GGG ACG CTG CAG CTC TAC CCC TTC TCC CCC TCC GCC TTC AAT AGC TTT  383

 I   H   D   N   D   Y   F   C   T   A   E   N   A   A   G   K   I   R   S   P   115
ATC CAC GAC AAT GAC TAC TTC TGC ACC GCG GAG AAC GCT GCC GGC AAG ATC CGG AGC CCC  443

 N   I   R   V   K   A   V   F   R   E   P   Y   T   V   R   V   E   D   Q   R   135
AAC ATC CGC GTC AAA GCA GTT TTC AGG GAA CCC TAC ACC GTC CGG GTG GAG GAT CAA AGG  503

 S   M   R   G   N   V   A   V   F   K   C   L   I   P   S   S   V   Q   E   Y   155
TCA ATG CGT GGC AAC GTG GCC GTC TTC AAG TGC CTC ATC CCC TCT TCA GTG CAG GAA TAT  563

 V   S   V   V   S   W   E   K   D   T   V   S   I   I   P   E   N   R   F   F   175
GTT AGC GTT GTA TCT TGG GAG AAA GAC ACA GTC TCC ATC ATC CCA GAA AAC AGG TTT TTT  623

 I   T   Y   H   G   G   L   Y   I   S   D   V   Q   K   E   D   A   L   S   T   195
ATT ACC TAC CAC GGC GGG CTG TAC ATC TCT GAC GTA CAG AAG GAG GAC GCC CTC TCC ACC  683

 Y   R   C   I   T   K   H   K   Y   S   G   E   T   R   Q   S   N   G   A   R   215
TAT CGC TGC ATC ACC AAG CAC AAG TAT AGC GGG GAG ACC CGG CAG AGC AAT GGG GCA CGC  743

 L   S   V   T   D   P   A   E   S   I   P   T   I   L   D   G   F   H   S   Q   235
CTC TCT GTG ACA GAC CCT GCT GAG TCG ATC CCC ACC ATC CTG GAT GGC TTC CAC TCC CAG  803

 E   V   W   A   G   H   T   V   E   L   P   C   T   A   S   G   Y   P   I   P   255
GAA GTG TGG GCC GGC CAC ACC GTG GAG CTG CCC TGC ACC GCC TCG GGC TAC CCT ATC CCC  863

 A   I   R   W   L   K   D   G   R   P   L   P   A   D   S   R   W   T   K   R   275
GCC ATC CGC TGG CTC AAG GAT GGC CGG CCC CTC CCG GCT GAC AGC CGC TGG ACC AAG CGC  923

 I   T   G   L   T   I   S   D   L   R   T   E   D   S   G   T   Y   I   C   E   295
ATC ACA GGG CTG ACC ATC AGC GAC TTG CGG ACC GAG GAC AGC GGC ACC TAC ATT TGT GAG  983

 V   T   N   T   F   G   S   A   E   A   T   G   I   L   M   V   I   D   P   L   315
GTC ACC AAC ACC TTC GGT TCG GCA GAG GCC ACA GGC ATC CTC ATG GTC ATT GAT CCC CTT 1043

 H   V   T   L   T   P   K   K   L   K   T   G   I   G   S   T   V   I   L   S   335
CAT GTG ACC CTG ACA CCA AAG AAG CTG AAG ACC GGC ATT GGC AGC ACG GTC ATC CTC TCC 1103

 C   A   L   T   G   S   P   E   F   T   I   R   W   Y   R   N   T   E   L   V   355
TGT GCC CTG ACG GGC TCC CCA GAG TTC ACC ATC CGC TGG TAT CGC AAC ACG GAG CTG GTG 1163

 L   P   D   E   A   I   S   I   R   G   L   S   N   E   T   L   L   I   T   S   375
CTG CCT GAC GAG GCC ATC TCC ATC CGT GGG CTC AGC AAC GAG ACG CTG CTC ATC ACC TCG 1223

 A   Q   K   S   H   S   G   A   Y   Q   C   F   A   T   R   K   A   Q   T   A   395
GCC CAG AAG AGC CAT TCC GGG GCC TAC CAG TGC TTC GCT ACC CGC AAG GCC CAG ACC GCC 1283
```

FIG. 5

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 Q   D   F   A   I   I   A   L   E   D   G   T   P   R   I   V   S   S   F   S   415
CAG GAC TTT GCC ATC ATT GCA CTT GAG GAT GGC ACG CCC CGC ATC GTC TCG TCC TTC AGC  1343

 E   K   V   V   N   P   G   E   Q   F   S   L   M   C   A   A   K   G   A   P   435
GAG AAG GTG GTC AAC CCC GGG GAG CAG TTC TCA CTG ATG TGT GCG GCC AAG GGC GCC CCG  1403

 P   P   T   V   T   W   A   L   D   D   E   P   I   V   R   D   G   S   H   R   455
CCC CCC ACG GTC ACC TGG GCC CTC GAC GAT GAG CCC ATC GTG CGG GAT GGC AGC CAC CGC  1463

 T   N   Q   Y   T   M   S   D   G   T                                          465
ACC AAC CAG TAC ACC ATG TCG GAC GGC ACC                                         1493
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(SEQ ID NO:5)

(SEQ ID NO: 6)

FIG. 5

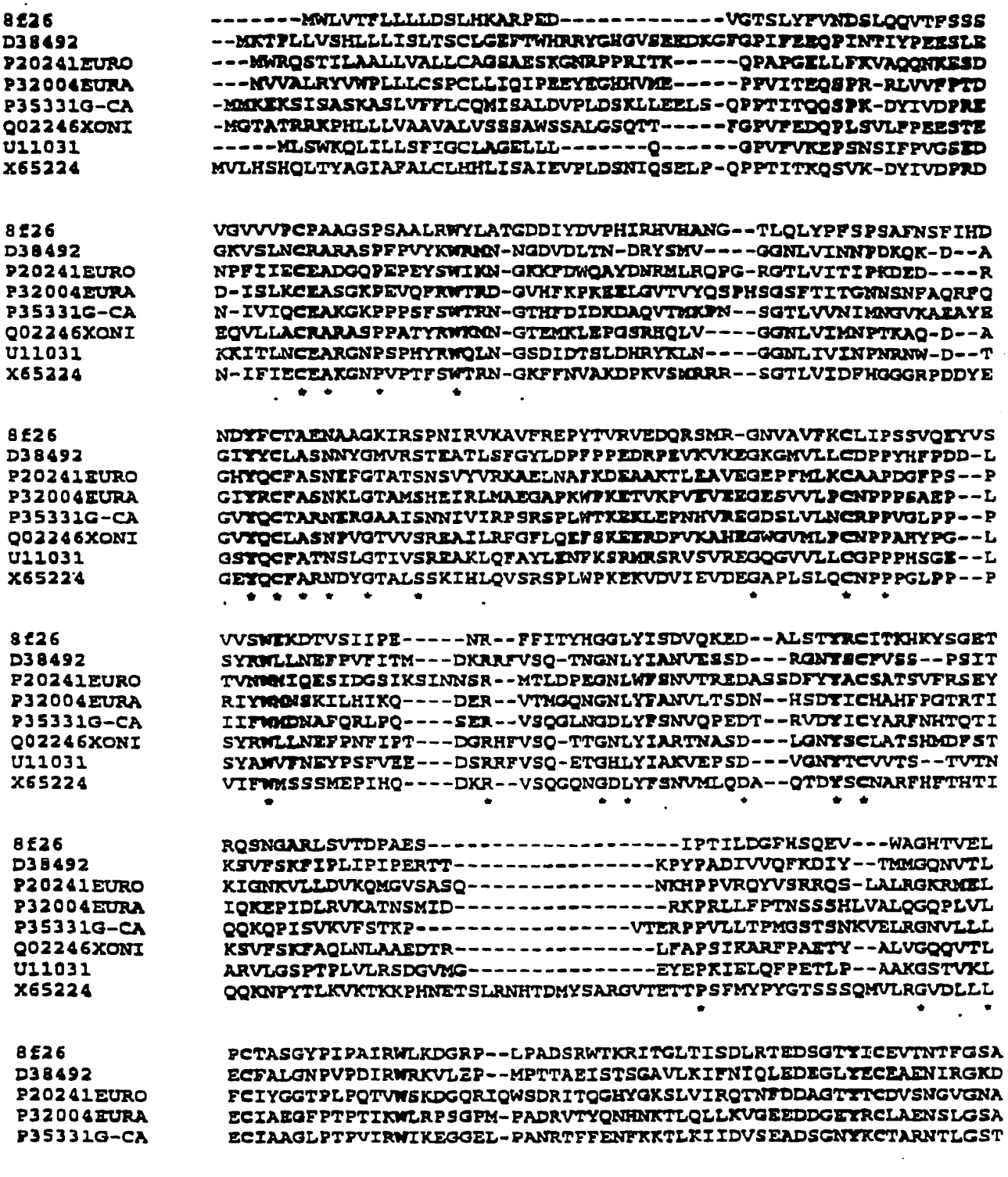
8f26
D38492
P20241EURO
P32004EURA
P35331G-CA
Q02246XONI
U11031
X65224

FIG. 6

```
Q02246XONI      ECFAFGNPVPRIKWRKVDG----SLSPQWTTAEPTLQIPSVSFEDEGTYECIAENSKGRD
U11031          ECFALGNPVPQINWRRSDGMP-FPTKIKLRRFNGVLEIPNFQQEDTGSYECIAENSRGKN
X65224          ECIASGVPAPDIMWYKKGGEL-PAGKTKLENFNKALRISNVSEEDSGEYFCLASNKMGSI

8f26            E-ATGILMVIDPLHVTLTPKKLKTGIGSTVILSCALTGSPEPTIRWYRNT----------
D38492          K-EQARIYVQAFPEWVEHINDTEVDIGSDLYWPCVATGKPIPTIRWLKNG----------
P20241EURO      QSFSIILNVNSVPYFTKEPEIATAAEDEEVVFECRAAGVPEPKISWIHNGKPIEQSTPNP
P32004EURA      R-HAYYVTVEAAPYWLHKPQSHLYGPGETARLDCQVQGRPQPEVTWRINGIPVEELAKDQ
P35331G-CA      H-HVISVTVKAAPYWITAPRNLVLSPGEDGTLICRANGNPKPSISWLTNGVPIAIAPEDP
Q02246XONI      T-VQGRIIVQAQPEWLKVISDTEADIGSNLRWGCAAAGKPRPTVRWLRNGEPLASQNR--
U11031          V-ARGRLTYYAKPYWVQLLKDVETAVEDSLYWECRASGKPKPSYRWLKNGDALVLEER--
X65224          R-HTISVRVKAAPYWLDEPQNLILAPGEDGRLVCRANGNPKPSIQWLVNGEPIEGSPPNP

8f26            ----E----------------------------LVLPDEAISIRGLSN----------
D38492          -YAYHKGELRLYDVTFENAGMYQCIAENAYGTIYANAELKILALAPTFEMNPMKKKILAA
P20241EURO      RRTVTDNTIRIINLVKGDTGNYGCNATNSLGYVYKDVYLNVQAEPP--TISEAPAAVSTV
P32004EURA      KYRIQRGALILSNVQPSDTMVTQCEARNRHGLLLANAYIYVVQLPA-KILTADNQTYMAV
P35331G-CA      SRKVDGDTIIFSAVQERSSAVYQCNASNEYGYLLANAFVNVLAEPP-RILTPANKLYQVI
Q02246XONI      -VEVLAGDLRFSKLSLEDSGMYQCVAENKHGTIYASAELAVQALAPDFRLNPVRRLIPAA
U11031          -IQIENGALTIANLNVSDSGMFQCIAENKHGLIYSSAELKVLASAPDFSRNPMKKMIQVQ
X65224          SREVAGDTIVFRDTQIGSSAVYQCNASNEHGYLLANAFVSVLDVPP-RILAPRNQLIKVI

8f26            ----------------------------------------ETLLITSAQKSHSGAYQCFA
D38492          KGGRVIIECKPKAAPKPKFSWSKGTEWLVNSSRILIWED-GSLEINNITRNDGGIYTCFA
P20241EURO      DGRNVTIKCRVNGSPKPLVKWLRASNWLT--GGRYNVQANGDLEIQDVTFSDAGKYTCYA
P32004EURA      QGSTAYLLCKAFGAPVPSVQWLDEDGTTVLQDERFFPYANGTLGIRDLQANDTGRYFCLA
P35331G-CA      ADSPALIDCAYFGSPKPEIEWFRGVKGSILRGNEYVFHDNGTLEIPVAQKDSTGTYTCVA
Q02246XONI      RGGEILIPCQPRAAPKAVVLWSKGTEILVNSSRVTVTPD-GTLIIRNISRSDEGKYTCFA
U11031          VGSLVILDCKPSASPRALSFWKKGDTVVREQARISLLND-GGLKIMNVTKADAGIYTCIA
X65224          QYNRTRLDCPFFGSPIPTLRWFKNGQGNMLDGGNYKAHENGSLEMSMARKEDQGIYTCVA

8f26            TRKAQTAQDFAIIALEDGTPRIVSSFSEKVVNPGEQFSLMCAAKGAP--PPTVTWALDDE
D38492          ENNRGKANSTGTLVITNPT-RIILAPINADITVGENATMQCAASFDPSLDLTFVWSFNGY
P20241EURO      QNKFGEIQADGSLVVKEHT-RITQEPQNYEVAAGQSATFRCNEAHDDTLEIEIDWWKDGQ
P32004EURA      ANDQNNVTIMANLKVKDAT-QITQGPRSTIEKKGSRVTFTCQASFDPSLQPSITWRGDGR
P35331G-CA      RNKLGKTQNEVQLEVKDPT-MIIKQPQYKVIQRSAQASFECVIKHDPTLIPTVIWLKD--
Q02246XONI      ENFMGKANSTGILSVRDAT-KITLAPSSADINLGDNLTLQCHASHDPTMDLTFTWTLDDF
U11031          ENQFGKANGTTQLVVTEPT-RIILAPSNMDVAVGESIILPCQVQHDPLLDIMFAWYFNGT
X65224          TNILGKVEAQVRLEVKDPT-RIVRGPEDQVVKRGSMPRLHCRVKHDPTLKLTVTWLKD--

8f26            PIVRDGSHRTNQYTMS----------------------------------------------(SEQ ID NO:7
D38492          VIDFNKEITNIHYQRNFMLDANGELLIRNAQLKHAGRYTCTAQTIVDNSSASADLVVRGP( "  8
P20241EURO      SIDFEAQPR-----FVKTNDN--SLTIAKTMELDSGEYTCVARTRLDEATARANLIVQDV( "  9
P32004EURA      --DLQELGD---SDKYFIEDG--RLVIHSLDYSDQGNYSCVASTELDVVESRAQLLVVGS( "  10
P35331G-CA      --NNELPDD----ERFLVGKD--NLTIMNVTDKDDGTYTCIVNTTLDSVSASAVLTVVAA( "  11
Q02246XONI      PIDFDKPGG--HYRRTNVKETIGDLTILNAQLRHGGKYTCMAQTVVDSASKEATVLVRGP( "  12
U11031          LTDFKKDGS--HFEKVGGSSS-GDLMIRNIQLKHSGKYVCMVQTGVDSVSSAAELIVRGS( "  13
X65224          --DAPLYIG----NRMKKEDD--GLTIYGVAEKDQGDYTCVASTELDKDSAKAYLTVLAI( "  14
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FIG. 6

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/20201

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07H 21/04; C07K 14/47; C12N 5/16, 15/70, 15/79; C12Q 1/68
US CL :435/6, 320.1, 325; 530/350; 536/23.5

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 172.3, 320.1, 325, 365; 530/350; 536/23.1, 23.5; 935/22, 24, 27, 79

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN (Biosis, CAPlus, LifeSci, Medline, INPADOC, WPIDS), Genbank, EMBL, Pir

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US, 5,525,486 A (HONJO et al.) 11 June 1996, see entire document.	1, 3, 4
A	US, 5,536,637 A (K. JACOBS) 16 July 1996, see entire document.	1, 3, 4

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

27 JANUARY 1998

Date of mailing of the international search report

23 FEB 1998

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